



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 115431

TO: Diana Johannsen
Location: REM/2C85
Art Unit: 1634
Monday, March 01, 2004

Case Serial Number: 09692077

From: Toby Port
Location: Biotech-Chem Library
Remsen 1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Johannsen,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 20:07:24 ; Search time 870 Seconds

(without alignments)
2540.799 Million cell updates/sec

Title: US-09-692-077D-1_COPY_880_930

Perfect score: 51

Sequence: 1 gagagtcgaagcgcgaagagga.....aggagagaggaagagagcgt 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 150 summaries

Database :

1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_ey:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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22: em_ov:*
23: em_pat:*
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29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
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35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_hcg_hum:*
39: em_hcg_mus:*
40: em_hcg_mus:*
41: em_hcg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	100.0	885	9	HUMA2C2	M38742 Human alpha
2	51	100.0	1030	9	HSR325747	AJ325747 Homo sapi
3	51	100.0	1353	6	AX350489	AX350489 Sequence
4	51	100.0	2072	6	AR270618	AR270618 Sequence
5	51	100.0	2072	6	HUMADRA2RA	M34041 Human alpha
6	51	100.0	3274	6	AX548756	AX548756 Sequence
7	51	100.0	9944	6	AF005900	AF005900 Homo sapi
8	43.6	85.5	133405	10	AL662790	AL662790 Mouse DNA
9	43.6	85.5	216444	2	AC069060	AC069060 Mus muscu
10	43.4	85.1	1185	10	ASP427259	AJ427259 Anomaliu
11	43.2	84.7	1183	4	OCYAR28	Y15946 Oryctolagus
12	43.2	84.7	1183	4	OCYAR28	Y16189 Oryctolagus
13	43.2	84.7	206933	2	AC108794	AC108794 Mus muscu
14	43.2	84.7	215065	2	AC103291	AC103291 Rattus no
15	43.2	84.7	222507	2	AC112440	AC112440 Rattus no
16	43.2	84.7	226214	2	AC126653	AC126653 Rattus no
17	43.2	84.7	287497	2	AC106946	AC106946 Rattus no
18	43.2	84.7	293183	2	AC095903	AC095903 Rattus no
19	43	84.3	1191	10	CCN427260	AJ427260 Castor ca
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21	42.6	83.5	232202	2	AC115740	AC115740 Mus muscu
22	42.2	82.7	31533	10	BX465209	BX465209 Mouse DNA
23	42.2	82.7	186272	10	AL672046	AL672046 Mus muscu
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25	42.2	82.7	189886	2	AC128202	AC128202 Rattus no
26	42.2	82.7	230127	10	AL691481	AL691481 Mouse DNA
27	42.2	82.7	230313	2	AC112634	AC112634 Rattus no
28	42.2	82.7	230313	2	AC120625	AC120625 Rattus no
29	42.2	82.7	268151	2	AC111391	AC111391 Rattus no
30	42	82.4	1198	4	ECAR28	Y15945 Equus caball
31	42	82.4	185321	2	AC110324	AC110324 Rattus no
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39	41.6	81.6	30837	2	AC126874	Continuation (5 of
40	41.6	81.6	42003	2	AC145716	AC145716 Homo sapi
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42	41.6	81.6	49999	6	AX015902	AX015902 Sequence
43	41.6	81.6	49999	6	AX015908	AX015908 Sequence
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50	41.6	81.6	136171	2	AC141946	AC141946 Rattus no
51	41.6	81.6	138191	8	BX842634	BX842634 Neurospor
52	41.6	81.6	141458	2	AC142044	AC142044 Rattus no
53	41.6	81.6	149814	10	AC130838	AC130838 Mus muscu
54	41.6	81.6	153176	2	AC132666	AC132666 Rattus no
55	41.6	81.6	153176	2	AC132666	AC132666 Rattus no
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57	41.6	81.6	154216	2	AC120503	AC120503 Didelphis
58	41.6	81.6	155094	2	AC122080	AC122080 Rattus no
59	41.6	81.6	155318	2	AC121661	AC121661 Rattus no
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63	41.6	81.6	161672	2	AC136667	AC136667 Rattus no
64	41.6	81.6	162738	9	AC083812	AC083812 Homo sapi
65	41.6	81.6	167787	2	AC109761	AC109761 Rattus no

Prod. No. is the number of results predicted by chance to have a

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C 69	41.6	81.6	172551	9	BS000152
C 70	41.6	81.6	174240	2	AC115905
C 71	41.6	81.6	175150	2	AC136657
C 72	41.6	81.6	177116	10	AC117249
C 73	41.6	81.6	177675	10	AC124534
C 74	41.6	81.6	178449	2	AC128251
C 75	41.6	81.6	181730	2	AC135151
C 76	41.6	81.6	185276	2	AC136050
C 77	41.6	81.6	185568	9	AC105227
C 78	41.6	81.6	187085	2	AC126944
C 79	41.6	81.6	187252	10	AL607109
C 80	41.6	81.6	189858	2	AC122382
C 81	41.6	81.6	191338	2	AC127650
C 82	41.6	81.6	192164	2	AC140220
C 83	41.6	81.6	193035	2	AC125186
C 84	41.6	81.6	194614	2	AC113594
C 85	41.6	81.6	196383	2	AC113159
C 86	41.6	81.6	197295	2	AC139652
C 87	41.6	81.6	198344	2	AC087872
C 88	41.6	81.6	198397	10	AC113021
C 89	41.6	81.6	199593	2	AL808137
C 90	41.6	81.6	202634	2	AC102541
C 91	41.6	81.6	205633	10	AL591496
C 92	41.6	81.6	206472	2	AC131874
C 93	41.6	81.6	207283	2	AC131874
C 94	41.6	81.6	207450	2	AC133255
C 95	41.6	81.6	210092	10	AC124563
C 96	41.6	81.6	210386	10	AL663065
C 97	41.6	81.6	211237	2	AC138325
C 98	41.6	81.6	211873	10	AL596122
C 99	41.6	81.6	212115	2	AC105773
C 100	41.6	81.6	212993	6	AX415544
C 101	41.6	81.6	215980	2	AC055773
C 102	41.6	81.6	217464	2	AC139061
C 103	41.6	81.6	218474	2	AC118179
C 104	41.6	81.6	219708	2	AC11854
C 105	41.6	81.6	220042	2	AC115901
C 106	41.6	81.6	220331	2	AC136625
C 107	41.6	81.6	220682	2	AC128616
C 108	41.6	81.6	223198	2	AC103014
C 109	41.6	81.6	223366	2	AC098602
C 110	41.6	81.6	224056	10	AC128832
C 111	41.6	81.6	226251	2	AC138033
C 112	41.6	81.6	227029	2	AC137871
C 113	41.6	81.6	227054	2	AC098956
C 114	41.6	81.6	227155	2	AC126640
C 115	41.6	81.6	228283	10	AF312994
C 116	41.6	81.6	228416	2	AC115254
C 117	41.6	81.6	232110	2	AC127946
C 118	41.6	81.6	232473	2	AC098461
C 119	41.6	81.6	233361	2	AC103428
C 120	41.6	81.6	233537	2	AC106105
C 121	41.6	81.6	233786	2	AC107140
C 122	41.6	81.6	233905	2	AC120465
C 123	41.6	81.6	234114	2	AC111449
C 124	41.6	81.6	234305	2	AC111938
C 125	41.6	81.6	235024	2	AC111938
C 126	41.6	81.6	235197	2	AC120681
C 127	41.6	81.6	236598	2	AC094766
C 128	41.6	81.6	236997	2	AC108239
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C 130	41.6	81.6	238355	2	AC113917
C 131	41.6	81.6	238818	2	AC103220
C 132	41.6	81.6	239901	2	AC111976
C 133	41.6	81.6	239808	2	AC126585
C 134	41.6	81.6	240145	2	AC097778
C 135	41.6	81.6	240247	2	AC133232
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C 137	41.6	81.6	241207	2	AC114861
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AC138595	Mus muscu
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BS000152	Pan trogl
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AC136657	Rattus no
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AC127650	Rattus no
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AL663065	Mouse DNA
AC138325	Mus muscu
AL596122	Mouse DNA
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AC055773	Mus muscu
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AC118179	Rattus no
AC11854	Rattus no
AC115901	Mus muscu
AC136625	Rattus no
AC128616	Rattus no
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143	41.6	81.6	243366	2	AC115313
144	41.6	81.6	244358	2	AC132065
145	41.6	81.6	244455	2	AC121672
146	41.6	81.6	247180	2	AC108653
147	41.6	81.6	247504	2	AC113220
148	41.6	81.6	247686	2	AC111776
149	41.6	81.6	248458	2	AC105827
150	41.6	81.6	249122	2	AC135438

ALIGNMENTS

RESULT 1	HUMA2C2	885 bp	DNA	linear	PRI 06-MAR-1995
LOCUS	HUMA2C2				
DEFINITION	Human alpha-2 adrenergic receptor (ADRA2C) gene, partial cde.				
ACCESSION	M38742.1				
VERSION	M38742.1				
KEYWORDS	alpha-2 adrenergic receptor.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	Chang, A.C., Ho, T.F., and Chang, N.C.				
TITLE	In vitro amplification by polymerase chain reaction of a partial gene encoding the third subunit of alpha-2 adrenergic receptor in humans				

Original source text: Human adult neuroblastoma DNA, clone PCRA2. Draft entry and computer-readable sequence for [Unpublished (1990)] by A.C.Chang, 20-SEP-1990.

Institute of Neuroscience
155, Sect II, Li-Noon St.
Taipei, Taiwan, 11221 ROC.

Location/Qualifiers
1..885

FEATURES
source

1..885

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Query Match
Best Local Similarity 100.0%; Score 51; DB 9; Length 885;
100.0%; Pred. No. 0.0017;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
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598 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 648

Db 1353 bp DNA linear PRI 18-JUL-2002
HSA325747/c
LOCUS Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION NBI-8185.
ACCESSION AJ325747
VERSION AJ325747.1 GI:15870141
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 Kurumaji, A.S., Gizaullin, R.Z., Al-Amin, A.N., Wang, F., Kvashe, S.M.,
Podewski, R.M., Matushkin, Y.G., Gyanchandani, A., Mutsaers, O.V.,
Levitky, V.G., Kolchanov, N.A., Protodopov, A.I., Kaashub, V.I.,
Kiselev, L.L., Wasserman, W., Mahlestedt, C. and Zabarovsky, E.R.
TITLE NotI flanking sequences: a tool for gene discovery and verification
of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PUBMED 12136098
REFERENCE 2 (bases 1 to 1030)
AUTHORS Zabarovsky, E.R.
TITLE Direct Substitution
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumourbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden

FEATURES
source 1..1030
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ORIGIN

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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1353 bp DNA linear PAT 06-FEB-2002
AX350489
LOCUS Sequence 1 from Patent WO0179561.
DEFINITION AX350489
ACCESSION AX350489
VERSION AX350489.1 GI:18616091
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Liggett, S.B. and Small, K.M.
TITLE Alpha-2 adrenergic receptor polymorphisms
JOURNAL Patent: WO 0179561-A 1 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten M. (US)
location/Qualifiers
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FEATURES
source

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2072 bp DNA linear PAT 10-APR-2003
AR270618
LOCUS Sequence 1181 from patent US 6500938.
DEFINITION AR270618
ACCESSION AR270618
VERSION AR270618.1 GI:29701852
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2072)
AUTHORS Au-Young, J. and Seilhamer, J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1181 31-DEC-2002;
location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 2072;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1292 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGT 1342

Db 2072 bp DNA linear PRI 30-OCT-1994
HUMADRA2RA
LOCUS Human alpha-2-adrenergic receptor (alpha-2 c2) gene, complete cds.
DEFINITION M34041
ACCESSION M34041
VERSION M34041.1 GI:178197
KEYWORDS alpha-2-adrenergic receptor; plasma membrane protein;
receptor-coupled G protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2072)
AUTHORS Lomasney, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W.,
Yang-Feng, T.L., Caron, M.G. and Lefkowitz, R.J.
TITLE Expansion of the alpha 2-adrenergic receptor family: cloning and
characterization of a human alpha 2-adrenergic receptor subtype,
the gene for which is located on chromosome 2
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
MEDLINE 90311349
PUBMED 2164221
COMMENT Original source text: Human placenta DNA, clone alpha-2 C2.
Draft entry and computer-readable sequence for (1) kindly submitted
by J.W.Lomasney, 03-MAY-1990, for release after publication.
location/Qualifiers
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FEATURES
source

[illegible]

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Burner, G.C., Pouch, C.L.
AUTHORS	

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/organism="Homo sapiens"
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/db_xref="taxon:9606"

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ACCESSION	Homo sapiens alpha2B-adrenergic receptor (alpha2C2AR) gene,
VERSION	AF005900 complete cds.
KEYWORDS	AF005900.2 GI:33435705
SOURCE	.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE		1 (bases 1 to 9944)	
AUTHORS		Cayla,C., Heinonen,P., Viikari,L., Schaak,S., Snapir,A., Bouloumie,A., Karvonen,M., Pesonen,U., Scheinin,M. and Paris,H.	
TITLE		Alpha2c2-adrenergic receptor gene	
JOURNAL		Unpublished	
REFERENCE		2 (bases 1 to 9944)	
AUTHORS		Cayla,C., Schaak,S., Bouloumie,A., Davedjian,J.C. and Paris,H.	
TITLE		Direct Submission	
JOURNAL		Submitted (29-MAY-1997) INSERM Unit 317, Institut Louis Bugnard,	
REFERENCE		3 (bases 1 to 9944)	
AUTHORS		Bouloumie,A., Karvonen,M., Pesonen,U., Scheinin,M. and Paris,H.	
TITLE		Direct Submission	
JOURNAL		Submitted (05-AUG-2003) INSERM Unit 317, Institut Louis Bugnard,	
REMARK		CHU Rangueil, Toulouse 31403, France	
COMMENT		Sequence update by submitter	
FEATURES		On Aug 5, 2003 this sequence version replaced gi:2245627.	
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ORIGIN	PolyA_signal	8751..8756	
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	Best Local Similarity	100.0%; Pred. No. 0.0015;	
	Matches	51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Dy	1 GAGATCAACCTGTAAGAGGAGAAGAGGAGAAGAGGAGAAGAGAGTGT	51	
Db	6379 GAGATGAAGCTGAAGAGAGGAGAGGAGAGGAGAGGAGAGAGTGT	6429	
RESULT 8	AL662790	133405 bp	DNA linear ROD 26-JUL-2002
LOCUS	AL662790		sequence.
DEFINITION	Mouse DNA sequence from clone RP23-53B2 on chromosome 11, complete		
ACCESSION	AL662790		
VERSION	AL662790.21	GI:22002673	
KEYWORDS	HTG.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Smith,M.		
REFERENCE	Submit Submission		
AUTHORS	Submitted (26-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK E-mail enquiries:		
TITLE			
JOURNAL			

Department of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen,
NETHERLANDS
On Nov 17, 1999 this sequence version replaced gi:3288559.
FEATURES
Source

Location/Qualifiers

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AKPLPLATPVASASANGSPKAGKEEETEDPTDLPGMATLPIPSGGQKEGV
SGASLEERAEEREEEREDERQAVPVSPASVSPLOQPOSRTLATIRGVLYGRC
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LF"

ORIGIN

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Best Local Similarity 93.8%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 48
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Db 845 GAGGAAGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 892

RESULT 12
LOCUS OCY16189 1183 bp DNA linear MM 02-JUL-1998
DEFINITION Oryctolagus cuniculus gene encoding alpha adrenergic receptor
subtype 2B, partial.
Y16189
Y16189.1 GI:3288561
alpha adrenergic receptor.
Oryctolagus cuniculus (rabbit)
SOURCE Oryctolagus cuniculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1
Stanhope,M.J., Madсен,O.J., Waddell,V.G., Claven,G.C., de Jong,W.M.
and Springer,M.S.
Highly congruent molecular support for a diverse superordinal clade
of edemic African mammals
Unpublished
2 (bases 1 to 1183)
Madsen,O.O.M.
Direct Submission
Submitted (12-JAN-1998) O.O.M. Madsen, University of Nijmegen,
Department of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen,
NETHERLANDS
FEATURES
Source

Location/Qualifiers

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/mol_type="genomic DNA"

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VGAMSGQWRRRAQLSRERKFTFLAVAVIGVFLCMFPFFSYSLAICPQCCRPVHG
LF"

ORIGIN

Query Match 84.7%; Score 43.2; DB 4; Length 1183;
Best Local Similarity 93.8%; Pred. No. 0.15; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 48
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Db 845 GAGGAAGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 892

RESULT 13
LOCUS AC108794/c 206933 bp DNA linear HTG 22-OCT-2002
DEFINITION Mus musculus clone RP23-59D8, WORKING DRAFT SEQUENCE, 10 ordered
pieces.
AC108794
AC108794.4 GI:24211386
HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Birren,B., Linton,L., Nussbaum,C., Lander,E., All,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bookhalter,B.,
Brown,A., Camarata,J., Campolano,A., Chang,J., Chazaro,B.,
Choquel,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gaidyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Huime,W., Huime,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kelle,C., LaRocque,K., Lamazeres,R.,
Lander,T., Lechoczky,J., Levine,R., Liu,G., Maclean,C.,
Maddonald,P., Major,J., Margus,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Melidrum,J., Meneus,J., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,D., Nguyen,C., Nicol,R., Notbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Roesti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Triggillo,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zaloun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (31-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 206933)

REFERENCE
AUTHORS Birren,B., Nussbaum,C., Lander,E., All,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Bookhalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choquel,Y., Collamore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gaidyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N.,
Hagos,B., Horton,L., Huime,W., Huime,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kelle,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Maclean,C., Maddonald,P., Major,J.,
Matthews,C., McCarthy,M., Melidrum,J., Meneus,J., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,D., Nguyen,C., Nicol,R., Notbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R.,
Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schuback,R.,

[illegible]

	* 211345	215065; contig of 3721 bp in length.
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ORIGIN		
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Matches	45; Conservative 0; Mismatches 3; Indels 0; Gaps 0.	
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Db	186041 GAGAGAAGAAGAAAGAAAGAAAGAGAAGAGAAGAGAAGAGAAG 186088	
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LOCUS	Rattus norvegicus clone CH230-14K15, WORKING DRAFT SEQUENCE, 4	
DEFINITION	unordered pieces.	
ACCESSION	AC112440	
VERSION	AC112440.5 GI:25006757	
KEYWORDS	HTG; HTGS PHASEI; HTGS DRAFT; HTGS_FULLTOP.	
SOURCE	Rattus norvegicus (Norway rat)	
ORGANISM	Rattus norvegicus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
REFERENCE	1 (bases 1 to 222507)	
AUTHORS	Muzny,D.,Marle,,Merzker,M.,Lee,,Abramzon,S.,Adams,C.,Alder,J., Allen,C.,Allen,H.,Alshrooke,S.,Amir,A.,Angiano,D., Anyalbechi,V.,Aoyagi,A.,Ayodeji,M.,Bac,E.,Baden,H., Baldwin,D.,Bandaranaike,D.,Barber,M.,Barnstead,M.,Benahmed,F., Blawie,K.,Blair,J.,Blankenburg,K.,Blyth,P.,Brown,M., Bryan,N.,Buha,Y.C.,Burck,B.,Butrell,K.,Calderon,E., Cardenas,V.,Carter,K.,Cavazos,I.,Ceasar,H.,Center,A., Chacko,J.,Chavez,D.,Chen,G.,Chen,R.,Chen,Y.,Chen,Z.,Chu J., Cleaveland,C.,Cockrell,R.,Cox,C.,Coyle,M.,Cree,A.,D'Souza,L., Devila,M.L.,Davis,C.,Davy-Carroll,L.,De Anda,C.,Dedrich,D., Delgado,O.,Denson,S.,Deramo,C.,Ding,Y.,Dinh,H.,Diya,K., Draper,H.,Dugan-Rocha,S.,Dunn,A.,Durbin,K.,Duval,B.,Eaves,K., Egan,A.,Escotto,M.,Eugene,C.,Evans,C.A.,Falls,T.,Fan,G., Fernandez,S.,Finley,M.,Flagg,N.,Forbes,L.,Foister,M.,Foister,P., Fraese,C.M.,Gabisi,A.,Ganta,R.,Garcia,A.,Garner,T.,Gaza,M., Georgeogis,E.,Geer,K.,Gill,R.,Grady,W.,Guerra,W.,Guevara,W.,	

COMMENT

Genome Center

Summary Statistics

AUTHORS

ORGANISMS

D6

ORIGIN

FEATURES

10

1

copy 880 9


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Consensus quality: 260614 bases at least Q30
Consensus quality: 263748 bases at least Q20
Estimated insert size: 265322; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/GenBank\_draft\_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence,
* as soon as it is available and the accession number will
* be preserved.
*
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* 1
* 97047: contig of 97047 bp in length
* 97048 97147: gap of unknown length
* 97148 101761: contig of 4614 bp in length
* 101762 101861: gap of unknown length
* 101862 254651: contig of 152790 bp in length
* 254652 254751: gap of unknown length
* 254752 258824: contig of 3473 bp in length
* 258825 258324: gap of unknown length
* 258325 271487: contig of 13165 bp in length
* 271488 271587: gap of unknown length
* 271588 276715: contig of 5128 bp in length
* 276716 276815: gap of unknown length
* 276816 278212: contig of 1397 bp in length
* 278213 278313: gap of unknown length
* 278313 280002: contig of 1690 bp in length
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* 281634 281733: gap of unknown length
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KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 293183)
Muzny,D,Marle, Metzger,M, Lee, Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alebrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Balwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhammed, F.,
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Deedrich, D.,
Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flegg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregiorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M.,
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowals, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenshew, L., Louised, H., Lozano, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,
Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Milosavljevic, A., Miner, G., Ming, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwaekelemeh, O., Okunolu, G., Olarnpusagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, A., Pfannkuch, C.,
Plopper, F., Polinder, A., Popovic, D., Primus, E., Pu, L., -L.,
Pua, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smales, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorrelle, R., Soosa, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabors, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uman, K.,
Valse, R., Vera, V., Villaseca, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhao, S., Zhao, S., Dunn, D., von
Niederhuesern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 293183)
Worley, K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 293183)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (13-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:2272685.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

----- Project Information
Center project name: GDVC
Center clone name: CH230-10L19

----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 227421 bases at least Q40
Consensus quality: 229231 bases at least Q30
Consensus quality: 230603 bases at least Q20
Estimated insert size: 234846; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 44341: contig of 44341 bp in length
* 44342 44342: gap of unknown length
* 44442 44442: gap of 3901 bp in length
* 48343 48343: gap of unknown length
* 48443 48443: gap of 241035 bp in length
* 289478 289478: gap of unknown length
* 289578 289578: gap of unknown length
* 291427 291427: gap of 1849 bp in length
* 291527 291527: gap of unknown length
* 293183 293183: contig of 1657 bp in length.
----- Location/Qualifiers
1. 293183
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-10L19"
9810. 10659
/note="clone boundary
clone_end:17
site:
end sequence: BH307090"
44442. 46192
/note="wgs_contig"
48443. 51434
/note="wgs_contig"
181343. 182203
/note="clone boundary
clone_end:5p6
site:
end sequence: BH307132"
231098. 232521
/note="wgs end-extension
clone_end:5p6"

ORIGIN

Query Match 84.7%; Score 43.2; DB 2; Length 293183;
Best Local Similarity 93.8%; Pred. No. 0.11;
Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Page 3

RESULT 20	AC115724/c	LOCUS	AC115724	217323 bp	DNA	linear	HMG 22-bp
DEFINITION	Mus musculus clone pnc 282						

Accession: AF057201.1, Working Draft Sequence, 6 unordered
 pieces.
 Version: AC115724
 Keywords: HTG, HTGS_PHASE1, HTGS_DRAFT.
 Source: Mus musculus (house mouse)
 Organism: Mus musculus

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

1 (bases 1 to 217333)
Birren, B., Nusbam, C. and Lander, E.
Mus musculus, clone RP23-20L18
Unpublished
2 (bases 1 to 217323)
Birren, B., Linton, J., Nusbam, C. and Lander, E.
Mus musculus, clone RP23-20L18
Unpublished

Anderson, S., Bernal, J., Musbaum, C., Lander, E., Ali, A., Allen, N.,
Bouhassira, D., Borna, N., Bastien, V., Bloom, T., Boguski, L.,
Chazaro, B., Chopel, Y., Colangelo, M., Campolongo, A., Chang, J.,
Cook, A., Cooke, J., Colangelo, M., Collins, A., Chang, J.,
Rao, S., Ferreira, P., DeRellano, K., Dewar, K., Diaz, J. S., Dode, S.,
Ginde, S., Gord, S., Goyette, M., Gage, D., Galagan, J., Gardyna, S.,
Hagos, B., Horton, L., Hulme, W., Hulme, I., Johnson, R., Jones, C.,
Kamat, A., Karas, A., Keijs, C., LaRoque, K., Lamazares, R.,
Landers, T., Lechoczky, J., Levine, R., Lindblad, T., Liu, G.,
McLellan, C., Macdonald, P., Major, J., Margulis, K., Liu, G.,
McCarthy, T., McEwan, P., McKernan, K., Meldrum, S.,
Mihova, T., Mlenaga, V., Murphy, T., Naylor, J., Matthews, C.,
Norbu, C., Norman, C. H., O'Connor, T., Nguyen, C., Nicol, R.,
Olivier, J., Peterson, K., Plunhanch, P., Pieter, N., Pollara, V.,
Raymond, C., Retts, R., Riedback, M., Riley, R., Rice, C.,
Roman, J., Rossetti, R., Riedback, M., Riley, R., Rice, C.,

SEAN, S., SEECTER, M., ROY, A., SANTOS, R., SCHAUER, S., KOGOV, P., STRAUSS, N., STEERY, P., SPENCER, B., STANGE-THOMANN, N., STOJANOVIC, N., TOPHAM, K., SUBRAMANIAN, A., TALMAZ, J., TESTAGE, S., STOJANOVIC, N., VIEL, R., VO, A., TRAVIS, M., TRAVIS, N., TRIGLIO, J., VASSILIEV, H., ZAINOUN, J., ZIMMEL, L., ZIMMER, A., WYMAN, D., YE, W.-J., YOUNG, G., Direct Submission
Submitted (32-MAR-2002) Whitehead Institute/MIT Center for Genome Research 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 317523)
B. Birren, Mph

Andeesson, S., Arachchi, L., Lander, E., Abouelella, A., Allen, N.,
 Bogdanavicius, L., Bouknight, H.M., Barna, N., Bastien, V., Bloom, T.,
 Collymore, A., Cook, A., Cooke, P., Corum, B., Chang, J., Choepel, Y.,
 Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Eckert, L., K.,
 Ferreira, P., Fitzgerald, M., Gage, D., Galban, J., Gardyna, S.,
 Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hages, B.,
 Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kama, A., Karic, A., Kells, C., Lander, E., Levine, R.,
 Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C.,
 Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
 Meldrum, J., Meneses, L., Mihova, T., Mieng, V., Murphy, T.,
 Nguyen, C., Nicol, R., Nordby, C., O'Connor, T., O'Donnell, P.,
 O'Neil, D., Oliver, R., Peterson, K., Phunhkanh, P., Pierre, N.,
 Rachupka, A., Ramasamy, U., Raymond, K., Phunhkanh, P., Pierre, N.,
 Rothen, J., Schauer, S., Schnuppach, R., Seaman, S., Severy, P.,
 Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
 Talamas, J., Teesdale, S., Theodore, J., Topham, K., Travers, M.,
 Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
 Wyman, D., Young, G., Zainoun, J., Zemlok, L., Zimmer, A. and Zody, M.,
 Direct Submission
 Submitted (22-FEB-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street Cambridge, MA 02141, USA
 On Feb 22, 2003 this sequence version replaced 91:2841066.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu>

[illegible]

RESULT 25	AC128202/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
	AC128202	169886 bp	DNA					
		Rattus norvegicus clone CH230-422P19, ***	linear					
			HTG 20-NOV-2005					
			SEQUENCING IN PROGRESS					
	AC128202	***, 2 unordered pieces.						
	AC128202.3	GI:25139218						
		HTG; HTGS PHASE1: HTGS_DRAFT; HTGS_ENRICHED.						
		Rattus norvegicus (Norway rat)						
		Rattus norvegicus						

REFERENCE AUTHORS

1 (bases 1 to 18986)

Muzny D, Mearns, Metzker, M, Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angilano, D., Anylebedich, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Batwala, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calerton, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Cetera, A., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Arna, C., Dederlich, D., Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Fraser, C. M., Gebail, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gedegeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Gunaratne, P., Haaland, W., Hamli, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hollins, B., Howells, S., Huylk, S., Hume, J., Idebladt, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolyet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., Kling, L., Kovar, C., Kowls, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewer, L., Louissege, H., Lozada, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindrasek, M., Mahmood, M., Malloy, K., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Manning, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,

TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 189886)
AUTHORS	Morley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (19-JUL-2002) Human Genome Sequencing Center

REFERENCE
AUTHORS
TITLE
JOURNAL

of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 189886)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center

COMMENT

Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Natf, L.,
Narkave, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwokedi, O., Okunnu, G., Olarnpungsoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plapper, F., Polidexter, A., Popovic, D., Prims, E., Pu, L.,
Puzos, M., Quirio, J., Rachlin, E., Reeves, K., Reiser, M., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojars, A., Rose, M., Rose, R., Ruiz, S.,
Sanders, W., Savary, G., Scherer, S., Scott, C., Shatman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smajs, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Stearle, M., Strong, R., Sutton, A., Swatek, A., Taber, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uemari, K.,
Valas, R., Vera, V., Villasaana, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wlarczyk, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, Y., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 189886)
Worley K.C.

Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 189886)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23908157.

The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
unspanned sequence only contigs will be indicated in the feature
table.

Center: Baylor College of Medicine
Genome Center
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center Project name: CH2M
Center clone name: CH230-423p9

Summary Statistics
Assembly program: Phrap, version 0.990329
Consensus quality: 175673 bases at least Q40
Consensus quality: 177888 bases at least Q30
Consensus quality: 179000 bases at least Q20
Estimated insert size: 177546; sum-of-ctrls estimation
Quality coverage: 6x in Q20 bases; sum-of-ctrls estimation

NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_drat_data.html)
NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES	
*	1 188573: contig of 188573 bp in length
*	188574 188573: gap of unknown length
*	188674 189886: contig of 1213 bp in length.
source	Location/Qualifiers
	1..189886
	/organism="Rattus norvegicus"
	/mol_type="genomic DNA"
	/db_xref="taxon:10116"
	/clone="CH230-423P19"
misc_feature	1..1138
	/note="wge end_extension
	clone_end:17"
misc_feature	complement(4656..4851)
	/note="clone_boundary
	clone_end:17
	site:
misc_feature	end_sequence:BZ183964"
	176896..177814
	/note="clone_boundary
	clone_end:Sp6
	site:
	end_sequence:BZ183966"
	180485..182844
	/note="wge end_extension
	clone_end:Sp6"
misc_feature	182895..184020
	/note="wge end_extension
	clone_end:Sp6"
misc_feature	187017..188573
	/note="wge end_extension
	clone_end:Sp6"

	Query Match	82.7%	Score 42.2;	DB 2;	Length 189886;
	Best Local Similarity	93.6%	Pred. No. 0.2;		
Matches	44;	Conservative	0;	Mismatches	3; Indels 0; Gaps 0;
QY	1	GAGCATGAAGCTGAAAGAGAGAGAAGAGAGAGAGAGAGAGAGA	47		
Db	167288	GAGGAGGAAGAGAGAGAGAGAGAGAAGAGAGAGAGAGAGAGAGA	167242		

AL691481	AL691481	230127 bp	DNA	linear	ROD 26-MAR-2003
LOCUS					
DEFINITION	Mouse DNA sequence from clone RP23-173C3 on chromosome 4. Contains a muscle enolase 3 beta (Eno3) pseudogene, a mitochondrial H+ transporting ATP synthase F0 complex subunit d (Atp5h) pseudogene and a CpG island, complete sequence.				
ACCESSION	AL691481				
VERSION	AL691481.15	GI:22213670			
KEYWORDS	HTG; Atp5h; CpG Island; Eno3.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eumariyoti; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 230127)				
AUTHORS	Tracey, A.				
TITLE	Direct Submission				
JOURNAL	Submitted (17-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk On Aug 13, 2002 this sequence version replaced gi:21748253.				
COMMENT	----- Genome Center Center: UK Medical Research Council Center code: UK-MRC Web site: http://micseq.har.mrc.ac.uk Contact: mouse@har.mrc.ac.uk				

During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information from the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

RP23-173C3 is from the RPc1-23 Mouse BAC Library constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBac3.6

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

This sequence is the entire insert of clone RP23-173C3 The true left end of clone RP23-426U14 is at 226462 in this sequence.

Location/Qualifiers

1..230127

FEATURES

source

```

misc_feature      22..695
                  /note="match: GSS: Em:AZ561521"
repeat_region     898..949
                  /note="26.0 copies 2 mer TG 86% conserved"
repeat_region     complement(956..1118)
                  /note="33A repeat: matches 8..178 of consensus"
repeat_region     1139..1156
                  /note="4.5 copies 4 mer TTTA 23% conserved"
repeat_region     1183..1193
                  /note="2.2 copies 5 mer TTATT 22% conserved"
repeat_region     1253..1285
                  /note="6.6 copies 5 mer TTTTC 34% conserved"
repeat_region     1258..1284
                  /note="3.0 copies 9 mer CTTTTC TTT 38% conserved"
repeat_region     1260..1275
                  /note="4.0 copies 4 mer TTTC 23% conserved"
repeat_region     1268..1295
                  /note="28.0 copies 1 mer T 20% conserved"
repeat_region     complement(1344..2435)
                  /note="11 repeat: matches 3332..5048 of consensus"
repeat_region     complement(12570..12768)
                  /note="11 repeat: matches 4623..4828 of consensus"
repeat_region     2805..2816
                  /note="2.4 copies 5 mer TACTA 24% conserved"
repeat_region     2956..2970
                  /note="2.5 copies 6 mer TTTGAT 21% conserved"
repeat_region     4183..4193
                  /note="2.2 copies 5 mer AGGA 22% conserved"
repeat_region     4943..4989
                  /note="3.9 copies 12 mer AGAAGAGACAG 49% conserved"
repeat_region     4953..4962
                  /note="5.0 copies 2 mer AG 20% conserved"
repeat_region     4996..5007
                  /note="2.4 copies 5 mer AAATG 24% conserved"
repeat_region     5069..5083
                  /note="3.0 copies 5 mer AGTGA 21% conserved"
repeat_region     complement(5128..5791)
                  /note="12 repeat: matches 2228..2955 of consensus"
repeat_region     6700..6713
                  /note="2.0 copies 7 mer ATCATTC 28% conserved"

```


TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL

Maheshwari, M., Mahindaratne, M., Mahmood, M., Mallory, K., Mangum, A., Mangum, B., Megue, P., Martin, K., Martin, R., Martinez, E., Maxwell, S., McLeod, M.P., McKell, T.Z., Meenen, E., Milobavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nakkeris, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokilemeh, O., Okunolu, G., Olampunsgoon, A., Pal, S., Parke, K., Paternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plöpper, F., Polndexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shivratheym, A., Sisson, I., Slitter, C.D., Smajz, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trujillo, Z., Umani, K., Valdes, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, Q., Wang, S., Warren, J., Warren, M., Wei, X., White, F., Williams, G., Willson, R., Wiczzyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederstockern, A., Weiser, R., Smith, D.R., Holt, R.A., Smith, H.O., Weissrock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 230227)
Worley, K.C.
Direct Submission
Submitted (22-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 230227)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:2365745.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
Project information
Center project name: GSRO
Center clone name: CH230-122C23
Summary Statistics
Assembly program: Phrap; version 0.990129
Consensus quality: 218431 bases at least Q40
Consensus quality: 219953 bases at least Q30
Consensus quality: 220999 bases at least Q20
Estimated insert size: 221147; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_difc_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct given, however the sizes

```

* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 230227: contig of 230227 bp in length.
FEATURES
    source
        1..230227
            /organism="Rattus norvegicus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10116"
            /clone="CH230-122C23"
            1..1370
                /note="wgs_end_extension
                clone_end:Sp6"
                /note="clone boundary
                clone_end:Sp6
                site:
                    end_sequence: BH267409"
                    226038..227375
                    /note="wgs_contig"
                    229157..230227
                    /note="wgs_contig"
ORIGIN
Query Match      82.7%  Score 42.2;  DB 2;  Length 230227;
Best Local Similarity 93.6%  Pred. No. 0.2;
Matches 44;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;
OY      1  GAGCATTGAGCTGAAGCAGCAGAAAGAGCAGAGCAGCAGCAGCAGAA 47
Db      121916 GAGCAGAGAAAGAAAGAGCAGAGAAAGAGCAGAGCAGCAGCAGAA 121962
AC120625
LOCUS      AC120625
DEFINITION Rattus norvegicus clone CH230-12B24, WORKING DRAFT SEQUENCE. 3
ACCESSION AC120625
VERSION    AC120625 4 GI:25137995
KEYWORDS   HTGS, HTGS_PHASE1, HTGS_DRAFT, HTGS_FULLTOP.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
1 (bases 1 to 230113)
Munry,D,Marle, Metzker,M,Lee, Abramzon,S, Adams,C, Alder,J.,
Allen,C, Allen,H, Alsbrooks,S, Amin,A, Anguiano,D,
Anyalabechi,V, Aoyagi,A, Ayodeji,M, Baca,E, Baden,H,
Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F,
Blawalo,K, Blair,J, Blankenburg,K, Blych,P, Brown,M,
Bryan,N, Buhay,C, Burch,P, Burrell,K, Calderon,E,
Cadenas,V, Carter,K, Cavazos,I, Ceasar,H, Centor,A,
Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
David,M,L, Davis,C, Davy-carroll,L, De Anda,C, Dederich,D,
Delgado,O, Denson,S, Deramo,C, Ding,Y, Dinh,H, Diya,K,
Drajer,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Eaves,K,
Egan,A, Escotto,M, Eugene,C, Evans,C, Falla,T, Fan,G,
Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P,
Freiser,C,M, Gabisi,A, Gante,R, Garcia,A, Garner,T, Guevara,W,
Gobregorgis,E, Geer,K, Gill,R, Grady,M, Guerra,M, Guetara,W,
Gunartne,P, Haland,W, Hamill,C, Hamilton,C, Hamilton,K,
Harvey,Y, Havlak,P, Hawes,A, Henderson,N, Hernandez,J,
Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M,
Hollins,B, Howell,S, Hulik,S, Hume,J, Idlebird,D, Jackson,A,
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Karpathy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Koyar,C,
Kovis,C, Kraft,C,L, Lebow,H, Levan,J, Lewis,D, Li,Z, Liu,J,
Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J,

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Unpublished
2 (bases 1 to 230313)

rdc genome Sequencing Consortium.
Direct Submission

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM

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----- Summary Statistics
Assembly program: phran: v0001
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NOTE: Estimated insert size may
(see <http://www.haac-bcm.tmc>)

AT PROOF CORRECT

Source

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[illegible]

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LOCUS
DEFINITION

VERSION	AC
1.0	1.0

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Date:

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Fertilization

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* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* As soon as it is available and the accession number will
* be preserved.
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1      227909: contig of 227909 bp in length
*      227910 228009: gap of unknown length
*      228010 229122: contig of 1113 bp in length
*      229123 229222: gap of unknown length
*      229223 230313: contig of 1091 bp in length.
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1 GAGCAGTAACTGAAGAAGGAGGAAGGAGGAGGAGGAGGAGGAACA 47
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AC111391      268151 bp       DNA         linear     HTG 13-MAY-2003
Rattus norvegicus clone CH230-14SD10, WORKING DRAFT SEQUENCE, 10
unnumbered pieces.
AC111391
AC111391.4 GI:30578964
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 268151)
Muzny,D.,Marie.,Metzker,M.,Lee.,Abramzon,S.,Adams,C.,Alder,J.,
Allen,C.,Allen,H.,Alsbrooks,S.,Amin,A.,Anguiano,D.,
Anyalabechi,V.,Aoyagi,A.,Ayodeji,M.,Baca,E.,Baden,H.,
Balwin,D.,Bandaranaike,D.,Barber,M.,Barnstead,M.,Benahmed,F.,
Biswalo,K.,Blair,J.,Blankenburg,K.,Blythe,P.,Brown,M.,
Bryant,N.,Bahay,C.,Burn,P.,Burrell,K.,Bych,B.,Calderon,E.,
Cardenas,V.,Carter,K.,Cavazos,I.,Caesar,H.,Center,A.,
Chacko,J.,Chavez,D.,Chen,G.,Chen,R.,Chen,Y.,Chen,Z.,Chu,J.,
Cleland,C.,Cockrell,R.,Cox,C.,Coyl,M.,Crease,A.,D'Souza,L.,
Devila,M.L.,Davis,C.,Davy-Carroll,L.,De Anda,C.,Dederich,D.,
Delgado,O.,Denison,S.,Deramo,C.,Ding Y.,Dinh,H.,Divya,K.,
Draper,H.,Dugan-Rocha,S.,Dunn,A.,Durbin,K.,Duval,B.,Eaves,K.,
Egan,A.,Escotto,M.,Eugene,C.,Evans,C.,Falls,T.,Fan,G.,
Fernandez,S.,Finley,M.,Flagg,N.,Forbes,L.,Foster,M.,Foster,P.,
Fraser,C.M.,Gabisi,A.,Ganta,K.,Garcia,A.,Garner,T.,Garza,M.,
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Eukaryota; Metazoa; Cnidaria; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
1 Stanhope M.J., Madson A. 1987-1988

and Springer, M.S., Cleven, G.C., de Jong, W.W.,
Hibbly, G.

of edemic African mammals
Unpublished

Direct Submission
Submitted (16-DEC-1997) O. Madsen

Department of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen, NETHERLANDS

Submitted (15-NOV-1999) 0 Madison, WI, USA

On Nov 17, 1999 this sequence version replaced gi:3288140.
Location/Qualifiers
1 1102

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Query Match	82.4%	Score 42;	DB 4;	Length 1198;
Best Local Similarity	90.0%;	Pred. No. 0.31;		
Matches	45; Conservative	0; Mismatch		

[illegible]

Search completed: February 29, 2004, 22:17:19
Job time : 899 secs

RESULT 2

AAD04762

ID AAD04762 standard; DNA; 1353 BP.

XX AAD04762;

XX 04-JUL-2001 (first entry)

XX Human alpha2B-adrenoceptor (alpha2B-AR) gene.

XX Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
XX glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
XX norepinephrine; epinephrine; therapy; vascular contraction;
XX coronary artery; coronary heart disease; CHD; chronic angina pectoris;
XX acute myocardial infarction; AMI; Primmetal's variant; ds.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..1353

FT /tag= a
FT /product= "Human alpha2B-adrenoceptor (alpha2B-AR)
FT protein"

XX MO200129082-A1.

XX 26-APR-2001.

XX 20-OCT-2000; 2000MO-F1000913.

XX 22-OCT-1999; 99US-00422985.

XX (JUVNA-) JUVANTIA PHARMA LTD OY.

XX Snapir A, Helonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;
XX Scheinin M, Salonen JT, Tuomainen T, Lakka TA, Nyssönen K;
XX Salonen R, Kaahenen J, Valkonen V,

XX MPI; 2001-300318/31.

XX P-PSDB; AAE00990.

XX New DNA molecule encoding variant specific adrenoceptor protein with
XX deletion of specific amino acids located in the third intracellular loop
XX of the polypeptide, for treating vascular contraction of coronary
XX arteries.

XX Disclosure; Page 27-29; 37pp; English.

XX The present sequence is a gene encoding human alpha2B-adrenoceptor
XX (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element
XX (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino
XX acids (amino acids 294-311), located in the third intracellular loop of
XX the receptor polypeptide. Alpha2B-AR gene is located on chromosome 2.
XX Alpha2-AR mediate many of the physiological effects of the
XX catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-
XX adrenoceptor is useful for treating a mammal suffering from vascular
XX contraction of coronary arteries and a disease involving vascular
XX contraction of coronary arteries which is clinically expressed as
XX coronary heart disease (CHD), unstable chronic angina pectoris which is
XX clinically expressed as Primmetal's variant form or acute myocardial
XX infarction (AMI). Alpha2B-AR gene is used in gene therapy

XX Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 100.0%; Score 51; DB 5; Length 1353;

XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51

DB 880 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 930

RESULT 3

AAD4389

ID AAD4389 standard; DNA; 1353 BP.

XX AAD4389;

XX 13-DEC-2002 (first entry)

XX Human alpha-2B-adrenoceptor gene.

XX Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
XX hypertension; hypotensive; gene; ds.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..1353

FT /tag= a
FT /product= "Human alpha-2B-adrenoceptor protein"

XX MO200266617-A1.

XX 29-AUG-2002.

XX 13-FEB-2002; 2002MO-F1000113.

XX 20-FEB-2001; 2001FI-00000323.

XX (JURI-) JURILAB LTD OY.

XX Salonen J;

XX MPI; 2002-667063/71.

XX P-PSDB; AAE2634.

XX Determining a risk of hypertension and targeting treatment in a subject by
XX determining the pattern of alleles encoding a variant alpha-2-
XX adrenoceptor.

XX Disclosure; Page 27-29; 35pp; English.

XX The invention relates to a method for detecting a risk of hypertension by
XX determining the pattern of alleles encoding a variant alpha-2B-
XX adrenoceptor (AR) protein. The methods and compositions of the invention
XX are useful for detecting risks and targeting treatment for hypertension.
XX The kit is also useful for selecting for clinical drug trials testing the
XX antihypertensive effect of compounds. The present sequence is human alpha
XX -2B-adrenoceptor gene

XX Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 100.0%; Score 51; DB 6; Length 1353;

XX Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

ID AAO14151 standard; DNA; 2064 BP.

XX AAO14151;

XX 06-JAN-1992 (first entry)

XX Human alpha 2 beta adrenergic receptor gene.

XX Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.

XX Homo sapiens.

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Dd	1278	GAGCATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGCAAGTGTT				1328

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AC	AAT59499;
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DT	25-MAR-2003 (revised)
DT	06-MAY-1997 (first entry)
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DE	Human alpha-2b adrenergic receptor genomic DNA clone.
XX	
KW	Alpha-2b adrenergic receptor; adrenoreceptor; adrenaline; epinephrine;
KW	signal transduction; neurotransmitter; ligand; ss.
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OS	Homo sapiens.
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Key	Location/Qualifiers
FT	288..1751
CDS	/*tag= a
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PN	US5595880-A.
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PD	21-JAN-1997.
XX	
PF	22-OCT-1992; 92US-00965040.
XX	
PR	30-OCT-1989; 89US-00428866.
PR	30-MAY-1991; 91US-00707604.
XX	
XX	
PA	(SYNA-) SYNAPTIC PHARM CORP.
XX	
XX	
PI	Hartig PR, Weinshank RL;

XX WP1; 1997-107576/10.
DR P-PDSB; AAMW1804.
XX
PT Assay for alpha-2b adrenergic receptor ligands - using membranes of cells
X expressing recombinant receptor.
PS Disclosure; Fig 2A-E; 16pp; English.

A genomic DNA clone (AA75949) codes for human alpha-2b adrenergic receptor (AAMI1804), a member of the rhodopsin-like signal transducer family. It was isolated from a human spleen genomic library in the lambda vector Charon 28 by screening with a 1.6 kb fragment of the human 5-hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2B comprising DNA encoding the alpha-2B adrenoreceptor is deposited as ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2B adrenoreceptor in bacterial, yeast or mammalian cells; transfected Ltk+ cells, designated L-NGC-alpha-2B, are deposited as ATCC CRL 10275. Membranes of such cells can used in novel methods to identify drugs which specifically interact with, and bind to, the alpha-2B adrenergic receptor. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 U; 0 Other;
SO

Query Match 100.0%; Score 51; DB 2; Length 2064;
Best Local Similarity 100.0%; Pred. No. 0.00056;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGAGGTGAACCTGTAAGAAGGATGAAGCATCAACCACCGTCGCCGCATTGGTCCCAGTTTG

Db	1278	1328
RESULT 6	GAGGATGAAGCTGAGAGGAGAAAGAGGAGGAGGAGGAGT	51
ID	ACAA56583	
XX	ACAA56583 standard; cDNA; 2072 BP.	
AC	ACAA56583;	
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DT	06-JUN-2003	(first entry)
DE	Human signalling pathway polynucleotide probe SEQ ID NO 1181.	
KW	Human; probe; ss; array element; Parkinson's disease;	
KW	signalling pathway population; cancer; adenocarcinoma;	
KW	immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray;	
OS	Homo sapiens.	
PN	US6500938-B1.	
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PD	31-DEC-2002.	
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PF	30-JAN-1998; 98US-00016434.	
XX		
PR	30-JAN-1998; 98US-00016434.	
XX		
PA	(INCY-) INCYTE GENOMICS INC.	
XX		
FI	Au-Young J, Sellhammer JT;	
XX		
DR	WPI; 2003-352189/33.	
XX		
PT	Combination of polynucleotide probes, useful as array elements in a	
PT	microarray for monitoring the expression of a number of target	
PT	polynucleotides.	
XX		
PS	Claim 1; SEQ ID NO 1181; 65pp; English.	
XX		
CC	The invention relates to a combination which, comprises a number of	
CC	polynucleotide probes comprising a sequence selected from one of the 1490	
CC	sequences mentioned in the specification. The combination is useful as an	
CC	array element in a microarray for monitoring the expression of a number	

CC of target polynucleotides. The microarray is particularly useful in the
CC diagnosis and treatment of cancer and immunopathology and neuropathology.
CC The microarray is useful in diagnostics and treatment regimens, drug
CC discovery and development, toxicological and carcinogenicity studies,
CC forensics and pharmacogenomics. The microarray is also useful for
CC monitoring progression of diseases and for developing sophisticated
CC profiles for the effects of currently available therapeutic drugs. The
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC and genomic fragments and in research and diagnostic applications. The
CC array can detect changes in expression in a large number of genes coding
CC for different signaling pathway populations which can be used to diagnose
CC various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC and Parkinson's disease. The present sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ Sequence 2072 BP; 316 A; 705 C; 660 G; 391 T; 0 U; 0 Other;
Query Match 100.0%; Score 51; DB 7; Length 2072;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGATGAAGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
DB 1292 GAGGATGAAGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 1342
RESULT 7
ABZ42624
ID ABZ42624 standard; DNA; 3274 BP.
XX
AC ABZ42624;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related disease; proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burner GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
XX
P-PSDB; ABP81780.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections, and
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42623 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 3274 BP; 587 A; 979 C; 967 G; 741 T; 0 U; 0 Other;
Query Match 100.0%; Score 51; DB 7; Length 3274;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGATGAAGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 51
DB 880 GAGGATGAAGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 930
RESULT 8
AAS68926
ID AAS68926 standard; cDNA; 291 BP.
XX
AC AAS68926;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #4730.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
P-PSDB; ABG04739.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnosis, forensics, gene mapping, identification of mutations

[illegible]

XX Bax; Bax-resistance; cytosolic; fungicide; immunosuppressive; virucide;
KM vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
KM apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
KM neurodegeneration; cell death; ss.
XX Saccharomyces cerevisiae.
XX WO200264766-A2.
XX 22-AUG-2002.
XX 21-DEC-2001; 2001WO-EP015398.
XX 22-DEC-2000; 2000EP-00870318.
XX 04-JAN-2001; 2001EP-00870002.
XX 09-JAN-2001; 2001EP-00870003.
XX (JANC) JANSSEN PHARM NV.
XX Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;
XX WPI; 2002-667002/71.
XX P-PSDB; ABG93152.
XX
XX New isolated nucleic acid representing a synthetic BAX-gene, useful as
PT medication for treating, preventing and/or alleviating yeast or fungal
PT infections or proliferative disorders, or for preventing apoptosis in
PT certain diseases.
XX
XX Claim 36; Fig 1; 344pp; English.
XX
XX This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytosolic, fungicide, immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenous flora of humans and
CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polynucleotide associated with the Bax gene
CC described in the disclosure of the invention.
XX
XX Sequence 1721 BP; 501 A; 400 C; 341 G; 479 T; 0 U; 0 Other;
SQ
XX
XX Query Match 79.6%; Score 40.6; DB 6; Length 1721;
XX Best Local Similarity 91.5%; Pred. No. 0.2;
XX Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGA 47
DB 631 GAGGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 585

XX Human; nucleic acid associated protein; NAAp, stroke; AIDS; neurologic;
KM cancer; atherosclerosis; neurological; epilepsy; Huntington's disease;
KM developmental disorder; antiinflammatory; neuroprotective; thrombotic;
KM Cushing's syndrome; infection; gene therapy; cytosolic; anticonvulsant;
KM cerebroprotective; hypothyroidism; cell proliferative disorder; allergy;
KM gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 237..2444
XX /*tag= a
XX /product= "Human NAAp protein"
XX
XX WO2003006618-A2.
XX
XX 23-JAN-2003.
XX
XX 10-JUL-2002; 2002WO-US021971.
XX
XX 12-JUL-2001; 2001US-0305089P.
XX 12-JUL-2001; 2001US-0305104P.
XX 13-JUL-2001; 2001US-0305325P.
XX 13-JUL-2001; 2001US-0305390P.
XX 19-JUL-2001; 2001US-0306560P.
XX 20-JUL-2001; 2001US-0306594P.
XX 27-JUL-2001; 2001US-0308170P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Swarnakar A, Richardson TW, Warren BA, Griffin JA, Tang YT;
PI Yde H, Baughn MR, Emerling BM, Lal PG, Lu DM, Forsythe IU;
PI Ramkumar J, Li JX, Becha SD, Duggan BM, Sanjanwala MM, Lee EA,
PI Burford N, Elliott VS, Ison CH, Ding L, Borowsky ML, Yao MG,
PI Barroso I, Tran B, Walla NK, Hafalia AJA, Nguyen DB, Lu Y;
PI Arvidu CS;
XX
XX WPI; 2003-221732/21.
XX P-PSDB; AAE37016.
XX
XX New human nucleic acid associated proteins (NAAp), useful for diagnosing,
PT treating and preventing diseases or conditions associated with the
PT aberrant NAAp expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
PT infections.
XX
XX Claim 5; Page 232; 260pp; English.
XX
XX The invention relates to human nucleic acid associated proteins (NAAp)
CC and their corresponding nucleic acid sequences. The invention is useful
CC in diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of NAAp, such as cell
CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
CC disorders, or infections. It is also useful in assessing the effects of
CC exogenous compounds on the expression of nucleic acid and amino acid
CC sequences for which NAAp or its fragments are useful in screening
CC compounds for which acts as their agonist or antagonist. The microarray
CC is useful in monitoring or measuring protein-protein interactions, drug-
CC target interactions, and gene expression profiles. NAAp DNA is used in
CC gene therapy. The present sequence is human NAAp cDNA
XX
XX Sequence 2663 BP; 875 A; 497 C; 715 G; 576 T; 0 U; 0 Other;
SQ
XX
XX Query Match 79.6%; Score 40.6; DB 7; Length 2663;
XX Best Local Similarity 91.5%; Pred. No. 0.21;
XX Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGA 47
DB 930 GAGGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 976

XX	Murine; mouse; gene trap technology; gene trapped sequence; GTS;
KW	gene identification; functional genomic analysis; gene discovery;
KW	gene expression analysis; cross species hybridisation analysis;
KW	antisense inhibition; gene targeting; gene; ss.
OS	Mus sp.
XX	
XX	US2002161207-A1.
PD	31-OCT-2002.
XX	
XX	30-NOV-2000; 2000US-00728444.
PF	
PR	01-DEC-1999; 99US-0168360P.
XX	
PA	(FRIE/) FRIEDRICH G.
PA	(ZAMB/) ZAMBROWICZ B.
PA	(SAND/) SANDS A T.
XX	
PI	Friedrich G, Zambrowicz B, Sands AT;
DR	WPI, 2003-288124/28.
XX	
PT	New murine polynucleotides comprising gene trapped sequences, useful in
PT	functional genomic analysis, in the development of new therapeutic or
PT	diagnostic agents, for diagnostic gene expression analysis or for genetic
PT	manipulations.
XX	
PS	Claim 2; SEQ ID NO 146; 29pp; English.
XX	
CC	The present invention relates to novel murine cDNAs produced using gene
CC	trap technology. The OMNIBANK gene trapped sequences (GTSs) are
CC	individually identified novel genes, and are useful in functional genomic
CC	analysis, in the discovery and development of new therapeutic and
CC	diagnostic agents, for gene discovery, for diagnostic gene expression
CC	analysis, for cross species hybridisation analysis, and for genetic
CC	manipulations such as antisense inhibition or gene targeting. The
CC	polynucleotides of the invention are also useful for isolating cDNAs,
CC	genomic clones or full-length genes/polynucleotides, or their homologues,
CC	heterologues, paralogues or orthologues, that are capable of hybridising
CC	to one or more of the new murine polynucleotide sequences. The
CC	polynucleotides are also useful for identifying the coding regions of the
CC	murine genome, and as hybridisation probes. ABX90657-ABX91862 represent
CC	the murine GTSs of the invention. Note: The sequence data for this patent
CC	did not form part of the printed specification, but was obtained in
CC	electronic format directly from the USPTO web site at
CC	seqdata.uspto.gov/patseqidententry.html
XX	
SQ	Sequence 223 BP; 64 A; 31 C; 65 G; 48 T; 0 U; 15 Other;
XX	
Query Match	78.4%; Score 40; DB 7; Length 223;
Best Local Similarity	89.6%; Pcred No. 0.28;
Matches 43; Conservative	0; Mismatches 5; Indels 0; Gaps 0
Oy	1 GAGGATGAAGCTGAAGAGGAGGAAGGAGGAGGAGGAGGAGGAGGAG 48
Db	14 GAGGAGGAAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 61
XX	
RESULT 20	
ID	AA875432
XX	AA875432 standard; cDNA; 224 BP.
XX	
AC	AA875432;
XX	
DT	13-FEB-2002 (first entry)
XX	
DE	DNA encoding novel human diagnostic protein #11236.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW	food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX	

[illegible]

The invention describes an isolated NOVX polypeptide (I) comprising a sequence selected from a sequence (SI) of 1121, 635, 299, 1720, 176, 5633 CC 214, 395, 1098, 134, 427, 1333, 407, 806, 804, 1253, 382, 1043, 176, 5633 CC 506, 759, 390, 133, 215, 240, 1069, 116, 439, 1188, 477, 316, 1065, 284, 496 CC 305, 406, 360, 353, 280, 829 or 326 amino acids fully defined in the CC specification, and the mature form of SI. (I) is useful for treating or CC preventing a pathology associated with (I) in a subject, preferably CC human, or for identifying an agent that binds to (I), where the agent is CC a cellular receptor or a downstream effector. (I) is useful for treating or CC encoding (I) or an anti-(I)-antibody (V) is useful for treating or preventing CC disorders or syndromes such as autoimmune disease, allergies, Alzheimer's CC disease, stroke, Parkinson's disease, Huntington's disease, multiple CC sclerosis, addiction, anxiety, pain, diabetes, glomerulonephritis, CC systemic lupus erythematosus, asthma, scleroderma, graft versus host CC disease, pancreatitis, obesity, ulcers, anaemia, cancer, trauma, viral, CC bacterial or parasitic infections, cardiomyopathy, atherosclerosis, CC hypertension, acquired immunodeficiency syndrome (AIDS) or Crohn's CC disease. (I), (II) or (V) is useful in screening assays, detection assays CC (e.g., chromosomal mapping, tissue typing, forensic biology), predictive CC medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical CC trials and pharmacogenomic), and in methods of treatment (e.g., CC therapeutic and prophylactic). (II) is useful in gene therapy, to express CC (I), to detect NOVX mRNA or a genetic lesion in a NOVX gene, and to CC modulate NOVX activity. This sequence encodes a novel human NOV protein CC XX

Sequence 1178 BP: 321 A: 286 C: 345 G: 603 T: 1000

Query Match	78.4%	Score 40;	DB 7;	Length 1178;
Best Local Similarity	89.6%;	Pred. No. 0.29;		
Matches 43;	Conservative 0;	Mismatches 5;	Indels	

[illegible]

RESULT 25
AAC38547
ID AAC38547 standard; DNA; 1956 BP
XX

AC	AAC38547;
XX	
DT	17-OCT-2000 (first entry)
yy	

Arabidopsis thaliana DNA fragment SEQ ID NO: 21366

Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway promoter; termination sequence; ss.

Arabidopsis thaliana

EP1033405-A2

06-SEP-2000

25-FEB-2000; 2000EP-00301439

25-FEB-1999: 0911G-01310000

05-MAR-1999; 99US-0123180P
09-MAR-1999; 99US-0123180P

23-MAR-1999; 99US-0123548P
25 MAR 1999 99US-0125788P

23-MAR-1999; 99US-0126264P
29-MAR-1999; 99US-0126785P

R	01-APR-1999;	99US-0127462P.
R	06-APR-1999;	99US-0128234P

R	08-APR-1999;	99US-0128714P..
R	16-APR-1999;	99US-0128845D

R 19-APR-1999; 99US-0130077P.
R 21-APR-1999; 99US-0130077P.

23-APR-1999; 99US-0130449P.
99US-0130510P.

PR	23- <u>APR</u> -1999	99US-0130891P
PR	28- <u>APR</u> -1999	99US-0131446P
PR	30- <u>APR</u> -1999	99US-0132048P
PR	04- <u>MAY</u> -1999	99US-0133407P
PR	06- <u>MAY</u> -1999	99US-0134084P
PR	07- <u>MAY</u> -1999	99US-0134485P
PR	07- <u>MAY</u> -1999	99US-0134867P
PR	11- <u>MAY</u> -1999	99US-0138663P
PR	14- <u>MAY</u> -1999	99US-0134218P
PR	14- <u>MAY</u> -1999	99US-0134221P
PR	14- <u>MAY</u> -1999	99US-0134219P
PR	14- <u>MAY</u> -1999	99US-0134710P
PR	18- <u>MAY</u> -1999	99US-0134768P
PR	19- <u>MAY</u> -1999	99US-0134941P
PR	20- <u>MAY</u> -1999	99US-0135114P
PR	21- <u>MAY</u> -1999	99US-0135313P
PR	24- <u>MAY</u> -1999	99US-0135629P
PR	25- <u>MAY</u> -1999	99US-0136021P
PR	27- <u>MAY</u> -1999	99US-0136382P
PR	28- <u>MAY</u> -1999	99US-0136782P
PR	01- <u>JUN</u> -1999	99US-0137222P
PR	04- <u>JUN</u> -1999	99US-0137528P
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PR	08- <u>JUN</u> -1999	99US-0138094P
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PR	16- <u>JUN</u> -1999	99US-0139451P
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PR	18- <u>JUN</u> -1999	99US-0139461P
PR	18- <u>JUN</u> -1999	99US-0139462P
PR	18- <u>JUN</u> -1999	99US-0139463P
PR	18- <u>JUN</u> -1999	99US-0139763P
PR	21- <u>JUN</u> -1999	99US-0139871P
PR	22- <u>JUN</u> -1999	99US-0139899P
PR	23- <u>JUN</u> -1999	99US-0140033P
PR	24- <u>JUN</u> -1999	99US-0140334P
PR	28- <u>JUN</u> -1999	99US-0140655P
PR	29- <u>JUN</u> -1999	99US-0140823P
PR	30- <u>JUN</u> -1999	99US-0140991P
PR	01- <u>JUL</u> -1999	99US-0141847P
PR	01- <u>JUL</u> -1999	99US-0142154P
PR	06- <u>JUL</u> -1999	99US-0142205P
PR	06- <u>JUL</u> -1999	99US-0142390P
PR	09- <u>JUL</u> -1999	99US-0142603P
PR	13- <u>JUL</u> -1999	99US-0142820P
PR	13- <u>JUL</u> -1999	99US-0142877P
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PR	16- <u>JUL</u> -1999	99US-0144085P
PR	19- <u>JUL</u> -1999	99US-0144086P
PR	19- <u>JUL</u> -1999	99US-0144331P
PR	19- <u>JUL</u> -1999	99US-0144332P
PR	19- <u>JUL</u> -1999	99US-0144333P
PR	19- <u>JUL</u> -1999	99US-0144334P
PR	19- <u>JUL</u> -1999	99US-0144335P
PR	20- <u>JUL</u> -1999	99US-0144336P

PR	20-JUL-1999;	99US-0144884P
PR	21-JUL-1999;	99US-0144884P
PR	21-JUL-1999;	99US-0145086P
PR	21-JUL-1999;	99US-0145088P
PR	22-JUL-1999;	99US-0145085P
PR	22-JUL-1999;	99US-0145087P
PR	22-JUL-1999;	99US-0145089P
PR	22-JUL-1999;	99US-0145119P
PR	22-JUL-1999;	99US-0145118P
PR	23-JUL-1999;	99US-0145115P
PR	23-JUL-1999;	99US-0145224P
PR	26-JUL-1999;	99US-0145226P
PR	27-JUL-1999;	99US-0145913P
PR	27-JUL-1999;	99US-0145918P
PR	27-JUL-1999;	99US-0145919P
PR	04-AUG-1999;	99US-0147302P
PR	04-AUG-1999;	99US-0147302P
PR	09-AUG-1999;	99US-0147935P
PR	09-AUG-1999;	99US-0148111P
PR	11-AUG-1999;	99US-0148319P
PR	12-AUG-1999;	99US-0148311P
PR	13-AUG-1999;	99US-0148565P
PR	13-AUG-1999;	99US-0148684P
PR	16-AUG-1999;	99US-0149366P
PR	17-AUG-1999;	99US-0149175P
PR	18-AUG-1999;	99US-0149462P
PR	20-AUG-1999;	99US-0149722P
PR	20-AUG-1999;	99US-0149723P
PR	20-AUG-1999;	99US-0149929P
PR	23-AUG-1999;	99US-0149902P
PR	23-AUG-1999;	99US-0149930P
PR	25-AUG-1999;	99US-0150566P
PR	25-AUG-1999;	99US-0150864P
PR	26-AUG-1999;	99US-0151065P
PR	27-AUG-1999;	99US-0151066P
PR	27-AUG-1999;	99US-0151080P
PR	30-AUG-1999;	99US-0151103P
PR	31-AUG-1999;	99US-0151438P
PR	01-SEP-1999;	99US-0151930P
PR	07-SEP-1999;	99US-0152363P
PR	10-SEP-1999;	99US-0153070P
PR	13-SEP-1999;	99US-0153788P
PR	15-SEP-1999;	99US-0154018P
PR	16-SEP-1999;	99US-0154039P
PR	20-SEP-1999;	99US-0154779P
PR	22-SEP-1999;	99US-0155139P
PR	23-SEP-1999;	99US-0155486P
PR	24-SEP-1999;	99US-0155659P
PR	26-SEP-1999;	99US-0156468P
PR	29-SEP-1999;	99US-0156566P
PR	04-OCT-1999;	99US-0157117P
PR	05-OCT-1999;	99US-0157753P
PR	06-OCT-1999;	99US-0157665P
PR	07-OCT-1999;	99US-0158029P
PR	08-OCT-1999;	99US-0158232P
PR	12-OCT-1999;	99US-0158369P
PR	13-OCT-1999;	99US-0159233P
PR	13-OCT-1999;	99US-0159249P
PR	13-OCT-1999;	99US-0159285P
PR	14-OCT-1999;	99US-0159330P
PR	14-OCT-1999;	99US-0159330P
PR	14-OCT-1999;	99US-0159331P
PR	14-OCT-1999;	99US-0159617P

PR	4-OCT-1999;	99US-0159558P
PR	18-OCT-1999;	99US-0159564P
PR	21-OCT-1999;	99US-0160761P
PR	21-OCT-1999;	99US-0160767P
PR	21-OCT-1999;	99US-0160768P
PR	21-OCT-1999;	99US-0160770P
PR	21-OCT-1999;	99US-0160814P
PR	21-OCT-1999;	99US-0160815P
PR	22-OCT-1999;	99US-0160980P
PR	22-OCT-1999;	99US-0160981P
PR	22-OCT-1999;	99US-0160989P
PR	22-OCT-1999;	99US-0160994P
PR	25-OCT-1999;	99US-0161405P
PR	25-OCT-1999;	99US-0161406P
PR	26-OCT-1999;	99US-0161335P
PR	26-OCT-1999;	99US-0161336P
PR	26-OCT-1999;	99US-0161361P
PR	28-OCT-1999;	99US-0161920P
PR	28-OCT-1999;	99US-0161922P
PR	28-OCT-1999;	99US-0161933P
PR	29-OCT-1999;	99US-0162142P

Query Match 78.4%; Score 40; DB 3; Length 1956;
Best Local Similarity 89.6%; Pred. No. 0.29;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 GAGGATGAACCTGAAGAGGAGGAAGAGGAGGAGGAGAAGAG 48
 ||| |||| | ||||||| ||||||| ||||||| ||||||| ||||
Db 579 GACGAGGAAGAAAGAAGAGGAAGAAGAGGAGGAGGAGGAGAG 626

RESULT 26

ABT20256 standard; DNA; 2367 BP.

AC ABT20256;

DT 16-APR-2003 (first entry)

DE Aspergillus fumigatus essential gene #2614

KM Fungicide; cytostatic; essential gene; *Aspergillus fumigatus*; infection.
KM cancer; contamination; biofilm; antibody; immune response; ds.

OS *Aspergillus fumigatus*

PN WO200286090-A2.

PD 31-OCT-2002.

PF 23-APR-2002; 2002WO-US013142

PR 23-APR-2001; 2001US-0285697P
PR 27-APR-2001; 2001US-0287066P

PR 05-JUN-2001; 2001US-0295890P
PR 09-JUL-2001; 2001US-0303899P

PR 31-AUG-2001; 2001US-0316362P
XX

PA (ELL-I-) ELLIKA PHARM INC
XX

FI 01aug B, 11BIVOLT C, EROBINIA ARI, HU W, DEMISEUA SI/
XX

REF ID: A66567

PT fumigatus, useful for treating or preventing infections by *A. fumigatus*,

XX

XX XX

essential genes of *Aspergillus fumigatus*. The isolated nucleic acids of

Query Match	78.4%	Score 40	DB 7	Length 2367
Best Local Similarity	89.6%	Pred No. 0.29		
Matches 43	Conservative 0	Mismatches 5	Indels 0	

RESULT 28
ABK65237
ID ABK65237 standard; cDNA; 2663 BP.
XX

[illegible]

(MEND-) MENDEL BIOTECHNOLOGY INC.
(PILG/) PILGRIM M.
(CREE/) CREELMAN R.
(DUBE/) DUBBELT A. J.
(HEAR/) HEARD J.
(JIANG) JIANG C.
(KEDD/) KEDDIE J.

PA (ADAM/) ADAM L.
PA (RATC/) RATCLIFF O.
PA (REUB/) REUBER J L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (PINE/) PINEDA O.
PI Pilgrim M, Creelman R, Dubell AJ, Heard J, Jiang C, Keddie J,
PI Adam L, Ratcliffe O, Reuber JL, Riechmann JL, Yu G, Pineda O;
XX
DR WPI: 2002-292022/33.
DR P-PSDB; AAU93051.
XX
PT An isolated or recombinant polynucleotide used to produce a transgenic
PT plant.
XX
PS Claim 4; Page 388-393; 941pp; English.
XX
CC The invention relates to 1 of 232 isolated or recombinant polynucleotides
CC encoding an Arabidopsis thaliana transcription factor, their variants,
CC complements, fragments, or related polynucleotide with 31% to 95%
CC sequence identity, where the plant possesses an altered trait as compared
CC to a wild-type or reference plant, or the plant exhibits an altered
CC phenotype as compared to a wild-type or reference plant, or the plant
CC exhibits ectopic expression or altered expression of one or more genes
CC associated with a plant trait as compared to a wild plant. Also included
CC are a transgenic plant comprising the polynucleotides, a computer
CC readable medium having stored sequence information, and identifying a
CC homologous sequence from a database comprising a plurality of known plant
CC sequences comprising inputting sequence information selected from one of
CC 464 fully defined sequences given in the specification. The isolated or
CC recombinant polynucleotide is used for producing a plant having a
CC modified trait, the method comprising selecting a polynucleotide that
CC encodes a polypeptide or an antisense nucleic acid, inserting the
CC polynucleotide or antisense nucleic acid into an expression vector,
CC introducing the vector into a plant or a cell of a plant to overexpress
CC the polypeptide or antisense nucleic acid, thereby producing a modified
CC plant, and selecting for a modified trait (e.g. increased production of
CC agriculturally useful proteins or metabolic chemicals, pest tolerance,
CC environmental stress response (e.g. drought), microbial disease
CC resistance, herbicide resistance, seed and fruit yield, growth rate, leaf
CC and flower senescence and many other traits listed in the specification).
CC The present sequence is one of the 232 polynucleotides encoding an A.
CC thaliana transcription factor
XX
SQ Sequence 2663 BP; 836 A; 544 C; 625 G; 658 T; 0 U; 0 Other;
XX
Query Match 78.4%; Score 40; DB 6; Length 2663;
XX Best Local Similarity 89.6%; Pred. No. 0.29;
XX Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 48
DB 865 GATGACGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 912
ACD98382
ID ACD98382 et al.; cDNA; 2663 BP.
XX
AC ACD98382;
XX
DT 23-SEP-2003 (first entry)
XX
DE A. thaliana disease tolerance transcription factor cDNA, G1089.
XX
KW Plant; ss; gene; transcription factor; disease resistance; transgenic;
XX plant breeding; pathogens resistance; pests; resistance.
OS Arabidopsis thaliana.
XX
XX US2003046723-A1.
XX

PD 06-MAR-2003.
XX
XX 22-MAR-2000; 2000US-00533029.
PF
XX 22-MAR-2000; 2000US-00533029.
PR
XX
XX (HEAR/) HEARD J.
PA (BROU/) BROUN P.
PA (RIEC/) RIECHMANN J L.
PA (KEDD/) KEDDIE J.
PA (PINE/) PINEDA O.
PA (ADAM/) ADAM L.
PA (SAMA/) SAMANA R.
PA (ZHAN/) ZHANG J.
PA (YUGG/) YU G.
PA (RATC/) RATCLIFFE O.
PA (PIIG/) PILGRIM M.
PA (JIAN/) JIANG C.
PA (REUB/) REUBER L.
PI Heard J, Brown P, Riechmann JL, Keddie J, Pineda O, Adam L,
PI Samana R, Zhang J, Yu G, Ratcliffe O, Pilgrim M, Jiang C, Reuber L;
XX
DR WPI: 2003-521768/49.
DR P-PSDB; ABO43116.
XX
PT New transgenic plants comprising a recombinant gene that alters the
PT plant's disease tolerance or resistance, useful in plant breeding, e.g.
PT for generating plants with improved tolerance or resistance to diseases,
PT pests or pathogens.
XX
PS Claim 14; Page 45-46; 124pp; English.
XX
CC The invention relates to a transgenic plant, comprising a recombinant
CC polynucleotide that alters the plant's disease tolerance or resistance
CC when compared with the same trait of another plant lacking the
CC recombinant polynucleotide. The recombinant polynucleotide comprises a
CC nucleotide sequence, which encodes a polypeptide comprising at least 6
CC consecutive amino acids of any of 56 transcription factor proteins
CC appearing as ABO43093-ABO43148. Also included are altering the disease
CC tolerance or resistance of a plant (by: (a) transforming a plant with the
CC recombinant polynucleotide; (b) selecting the transformed plants; and (c)
CC identifying a transformed plant with an altered disease tolerance or
CC resistance), altering the expression levels of at least one gene in a
CC plant by transforming the plant with the recombinant polynucleotide,
CC altering a plant's trait (comprising: (a) providing a database sequence;
CC (b) comparing the database sequence with the polypeptide or
CC polynucleotide cited above; (c) selecting a database sequence that meets
CC the selected sequence criteria; and (d) transforming the selected
CC database sequence in the plant) and altering a plant's trait (comprising:
CC (a) providing a test polynucleotide; (b) hybridizing the test
CC polynucleotide at low stringency with the recombinant polynucleotide
CC cited above; and (c) transforming the hybridizing test polynucleotide in
CC a plant to alter a trait of the plant. The transgenic plant is useful in
CC plant breeding, particularly for generating plants with improved
CC tolerance or resistance to diseases. The plants have commercial utility
CC for increasing tolerance or resistance to pathogens and pests. The
CC present sequence is an Arabidopsis thaliana transcription factor cDNA of
CC the invention
XX
SQ Sequence 2663 BP; 836 A; 544 C; 625 G; 658 T; 0 U; 0 Other;
XX
Query Match 78.4%; Score 40; DB 8; Length 2663;
XX Best Local Similarity 89.6%; Pred. No. 0.29;
XX Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 48
DB 865 GATGACGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 912
ACD98382
ID ACD98382 et al.; cDNA; 2663 BP.
XX
AC ACD98382;
XX
DT 23-SEP-2003 (first entry)
XX
DE A. thaliana disease tolerance transcription factor cDNA, G1089.
XX
KW Plant; ss; gene; transcription factor; disease resistance; transgenic;
XX plant breeding; pathogens resistance; pests; resistance.
OS Arabidopsis thaliana.
XX
XX US2003046723-A1.
XX

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 14:57:29 ; Search time 2149 Seconds

(without alignments)
708.688 Million cell updates/sec

Title: US-09-692-077D-1_COPY_880_930

Perfect score: 51

Sequence: 1 gagagtgagcgcgaagagga.....aggagagaggaagagcgt 51

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gsa_hum:*
18: em_gsa_inv:*
19: em_gsa_pln:*
20: em_gsa_vrt:*
21: em_gsa_fun:*
22: em_gsa_mam:*
23: em_gsa_mus:*
24: em_gsa_pro:*
25: em_gsa_rtd:*
26: em_gsa_phg:*
27: em_gsa_vrt1:*
28: gb_gsa1:*
29: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	1353	29	AY16856 Homo sapi
2	42	87.2	29	ECMA2BAR	AL606560 Horse alp
3	41.6	81.6	430	28	AZ223727 RPI-23-6
4	41.6	81.6	469	9	AA943361 EST198860

5	41.6	81.6	517	10	BE097734	BE097734 UI-R-B01-
6	41.6	81.6	552	14	CF795982	CF795982 892192 MA
7	41.6	604	9	AJ517718	AJ517718 AJ517718	AJ517718
8	41.6	713	28	AZ288043	AZ288043 RPI-23-1	AZ288043 RPI-23-1
9	40.6	79.6	640	12	B1067787	B1067787 p9f1n.pko
10	40.6	79.6	668	28	BH309086	BH309086 CH230-4L1
11	40.6	79.6	723	13	BU121352	BU121352 603146064
12	40.6	79.6	753	10	BE613618	BE613618 601504406
13	40.6	79.6	797	28	AO875889	AO875889 V130F6 MT
14	40.6	79.6	826	28	B2227940	B2227940 CH230-400
15	40.6	79.6	873	13	BQ231724	BQ231724 AGENCOURT
16	40.6	79.6	1362	12	BM807097	BM807097 AGENCOURT
17	40.4	79.2	453	10	BB852469	BB852469 BB852469
18	40.4	79.2	553	13	BX519271	BX519271 BX519271
19	40.4	79.2	786	28	AZ208950	AZ208950 SP 0138-A
20	40.4	79.2	799	28	BZ152227	BZ152227 CH230-504
21	40.4	79.2	834	28	BZ249816	BZ249816 CH230-447
22	40.4	79.2	152	28	BH108383	BH108383 RPI-24-4
23	40.4	78.4	167	28	BH072396	BH072396 RPI-24-2
24	40.4	78.4	256	14	CA152228	CA152228 UI-M-FW0-
25	40.4	78.4	330	14	CF897938	CF897938 AO231H07-
26	40.4	78.4	331	9	AL135731	AL135731 DXFZP34H
27	40.4	78.4	358	14	CD564037	CD564037 B0473A03-
28	40.4	78.4	365	13	BY054209	BY054209 BY054209
29	40.4	78.4	365	13	BY168255	BY168255 BY168255
30	40.4	78.4	373	14	CA538239	CA538239 C0264C01-
31	40.4	78.4	388	13	BY135560	BY135560 BY135560
32	40.4	78.4	413	28	BZ105773	BZ105773 CH230-153
33	40.4	78.4	444	13	BQ558077	BQ558077 H4050A07-
34	40.4	78.4	446	10	BG076252	BG076252 H3157D11-
35	40.4	78.4	459	28	AZ554793	AZ554793 RPI-23-2
36	40.4	78.4	476	10	BB851808	BB851808 BB851808
37	40.4	78.4	512	14	CB272922	CB272922 ma164d07
38	40.4	78.4	514	28	BZ089457	BZ089457 CH230-1C1
39	40.4	78.4	517	14	CB716103	CB716103 AMGNNUC:N
40	40.4	78.4	558	28	BZ159900	BZ159900 CH230-376
41	40.4	78.4	578	14	CA752540	CA752540 UI-M-F00-
42	40.4	78.4	586	9	AI451753	AI451753 mb16f09.Y
43	40.4	78.4	587	12	BG325179	BG325179 602423735
44	40.4	78.4	594	14	CF796838	CF796838 NCSTqab8
45	40.4	78.4	612	28	BZ149404	BZ149404 CH230-395
46	40.4	78.4	615	28	AZ387057	AZ387057 IM0146P14
47	40.4	78.4	639	11	AY387076	AY387076 Raturus no
48	40.4	78.4	649	10	BB662759	BB662759 BB662759
49	40.4	78.4	668	10	BB048926	BB048926 BB048926
50	40.4	78.4	673	13	CB057694	CB057694 NISC-J607
51	40.4	78.4	677	13	BY706040	BY706040 BY706040
52	40.4	78.4	690	10	BB595707	BB595707 BB595707
53	40.4	78.4	701	13	BU547473	BU547473 GM880012A
54	40.4	78.4	711	13	BY741447	BY741447 BY741447
55	40.4	78.4	723	14	CF994084	CF994084 AGENCOURT
56	40.4	78.4	740	28	AZ940126	AZ940126 ZM0199F23
57	40.4	78.4	792	14	BZ268857	BZ268857 CH230-274
58	40.4	78.4	798	14	CB195753	CB195753 AGENCOURT
59	40.4	78.4	851	14	CA325188	CA325188 UI-M-FV0-
60	40.4	78.4	889	12	BG175332	BG175332 602337674
61	40.4	78.4	1047	13	BQ894173	BQ894173 AGENCOURT
62	40.4	78.4	1080	11	AK005900	AK005900 Mus muscu
63	40.4	78.4	1249	14	CB192954	CB192954 AGENCOURT
64	40.4	78.4	1595	11	AK008242	AK008242 Mus muscu
65	40.4	78.4	1596	11	AK010941	AK010941 Mus muscu
66	40.4	78.4	2379	11	AK047841	AK047841 Mus muscu
67	40.4	78.4	2771	11	AK086271	AK086271 Mus muscu
68	40.4	78.4	3439	11	AK082468	AK082468 Mus muscu
69	40.4	78.4	3890	11	AK036071	AK036071 Mus muscu
70	39.8	78.0	248	28	AZ552041	AZ552041 RPI-23-2
71	39.8	78.0	306	28	AZ382276	AZ382276 IM0139N15
72	39.8	78.0	354	14	CB961043	CB961043 AGENCOURT
73	39.8	78.0	408	13	BY670049	BY670049 BY670049
74	39.8	78.0	3128	11	AK041807	AK041807 Mus muscu
75	39.6	77.6	562	13	BQ830593	BQ830593 L161n1087
76	39.6	77.6	1045	13	BX425625	BX425625 BX425625
77	39.4	77.3	245	14	Z74660	Z74660 NMTC21 Mou

78	39.4	77.3	797	28	BH265596
79	39.2	76.9	799	14	CK140197
80	39	76.5	799	14	AA506305
81	39	76.5	169	29	CE313094
82	39	76.5	221	28	BH363723
83	39	76.5	266	12	BG795271
84	39	76.5	266	29	CE763075
85	39	76.5	295	28	BH294069
86	39	76.5	309	28	BH113907
87	39	76.5	310	14	CB988548
88	39	76.5	322	28	AQ930689
89	39	76.5	351	29	EM796809
90	39	76.5	353	13	BY140045
91	39	76.5	360	13	BY173203
92	39	76.5	392	9	A1558058
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ALIGNMENTS

RESULT 1
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AY16856
Homo sapiens HCM6030 gene, VIRTUAL TRANSCRIPT, partial sequence,
AY16856
AY16856.1 GI:39772816
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

1 (bases 1 to 1353)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Clavello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
1..1353
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/locus_tag="HCM6030"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 51; DB 29; Length 1353;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

ECOA2BAR
Horse alpha2 adrenergic receptor gene fragment probably subtype D,
AL060650
AL060650.1 GI:15591917
GSS; Alpha2 adrenergic receptor gene.
Equis caballus (horse)
Equis caballus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

1 (bases 1 to 872)
Hunter, C. and Elgar, G.
Alpha2 adrenergic receptor gene
Unpublished
2 (bases 1 to 872)
Hunter, C.
Direct Submission

RESULT 8
AZ288043/c
LOCUS
DEFINITION RPCI-23-102K10.TV RPCI-23 Mus musculus genomic clone
ACCESSION RPCI-23-102K10, genomic survey sequence.
VERSION A2288043
KEYWORDS A2288043.1 GI:9529829
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 713)
REFERENCE
AUTHORS Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatsman, S.,
Akintret, B., Levins, M., Megann, S., Tsegaye, G., Geer, K., Krol, M., de
Jong, P., and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
OTHER GSSes: RPCI-23-102K10.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pdejong@tigr.org, med.bu@fao.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.bu@fao.edu/orderingframe.htm>)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html
Plate: 102 row: K column: 10
Seq primer: T7
Classes: BAC ends.
FEATURES
source
1..713
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-102K10"
/sex="Female"
/lab_host="DH10B"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
ORIGIN
Query Match 81.6%; Score 41.6; DB 28; Length 713;
Best Local Similarity 91.7%; Pred. No. 46;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGAGGAGAGGAGAG 48
|||||
Db 101 GAGGAGGAAGAGAGGAGAGGAGGAAGAGGAGAGGAGAGGAGAGAG 54
|||||
RESULT 9
B1067787
LOCUS
DEFINITION B1067787 640 bp mRNA linear EST 15-JUN-2001
cdna clone pgfin.pk007.124 5' similar to gi|4506411
ref|NP_002874.1| Rat GRPase activating protein 1; Pngl (Homo
sapiens) gi|11418178 ref|XP_010014.1| Rat GRPase activating protein
1 (Homo sapiens) sp|P46060|RGPI_HUMAN RAT-GRPASE ACTIVATING PROTEIN
1 prt|I18146 RANGAPI - human pI|JC, mRNA sequence.
ACCESSION B1067787

VERSION B1067787.1 GI:14475309
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 640)
REFERENCE
AUTHORS Cogburn, L.A., Morgan, R.W., and Burnside, J.
Chicken ESTs from fat
Unpublished (2001)
TITLE
JOURNAL
COMMENT Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
1..640
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pgfin.pk007.124"
/sex="Male and Female"
/issue_type="fat"
/lab_host="E.coli EMDH108"
/clone_lib="normalized chicken fat cdna library"
/note="Vector: pSPORT1"
ORIGIN
Query Match 79.6%; Score 40.6; DB 12; Length 640;
Best Local Similarity 91.5%; Pred. No. 71;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGAGGAGAGGAGAGA 47
|||||
Db 180 GAAAGAGGATGAAGAGGAGGAAGAGGAGAGGAGAGGAGAGAGA 226
|||||
RESULT 10
BH309086/c
LOCUS
DEFINITION BH309086 668 bp DNA linear GSS 03-DEC-2001
CH230-4116, TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION BH309086
VERSION BH309086.1 GI:17234555
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 668)
REFERENCE
AUTHORS Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,
Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, P., de Jong, P., and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished (1999)
TITLE
JOURNAL
COMMENT Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(<http://www.chori.org/bacpac/rat230.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/orering_information.htm). BAC end
page: http://www.tigr.org/cdb/bac_ends/rat/bac_end_intro.html
Plate: 4 row: L column: 16
Seq primer: T7

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished (1999)
Contact: Kumar A
Michael Snyder, Dept. of Mol. Cell. and Dev. Biology
Yale University
P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
Email: anuj.kumar@yale.edu
te of mtb-3xHA/lacZ insertion.
Seq primer: GGCTCTCTTCTTGGAGTAC
Class: transposon-tagged.

FEATURES
source
1.797
/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/strain="Y2278 - S288C background, cir(0) rho(0)"
/db_xref="taxon:4932"
/lab_host="E. coli"
/clone_lib="mtb-3xHA/lacZ insertion library, strain Y2278"
/note="Vector: pHS6-Sal; A yeast genomic DNA library
without 2 micron or mitochondrial DNA was prepared in
pHS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mtb-3xHA/lacZ
multitransposon containing lacZ, URA3, and tetr resistance."

ORIGIN
Query Match 79.6%; Score 40.6; DB 28; Length 797;
Best Local Similarity 91.5%; Pred. No. 73;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OR
1 GAGGATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGA 47
260 GAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 306

RESULT 14
LOCUS B2227940/c 826 bp DNA linear GSS 12-OCT-2002
DEFINITION CH230-400D22.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
ACCESSION B2227940
VERSION B2227940.1 GI:23886481
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 826)
Zhao,S., Shetty,J., Shatman,S., Teegase,G., Geer,K.,
Shvartsbeyn,A., Gebregiorgis,E., Overton,L., Russell,D., Chen,D.,
Riggs,R., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@cihr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ordering information.html). BAC end
page: http://www.cihr.org/cdb/bac_ends/rat/bac_end_intro.html
Plate: 400 row: D column: 22
Seq primer: SP6
Class: BAC ends.

FEATURES
source
1.826
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SENHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-400D22"
/sex="Female"
/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SENHsd/MCW) BAC library produced by
Pieter de Jong"

ORIGIN
Query Match 79.6%; Score 40.6; DB 28; Length 826;
Best Local Similarity 91.5%; Pred. No. 73;
Matches 43; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OR
1 GAGGATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGA 47
794 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 748

RESULT 15
LOCUS BQ231724 873 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT 7560029 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6055864
5' mRNA sequence.

ACCESSION BQ231724
VERSION BQ231724.1 GI:20413124
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 873)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rmml.nih.gov
Tissue Procurement: ATCC/DCPD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1316 row: m column: 17
High quality sequence stop: 703.
Location/Qualifiers

FEATURES
source
1.873
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6055864"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: Skin; Vector: pCMV-SORT2; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

	Query Match	79.6%;	Score 40.6;	DB 13;	Length 873;	
	Best Local Similarity	91.5%;	Pred. No. 74;			
	Matches	43;	Conservative	0;	Mismatches	4; Indels 0; Gaps 0
Qy	1	GAGGATGAACCTGAAGAGAGAAGAGAGAGAGAGAGAGAGA	47			
Db	103	GAGAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	149			
RESULT 16						
Bm807097						
LOCUS	Bm807097	1362 bp	mRNA	linear	EST 05-MAR-2002	
DEFINITION	AGENCOURT_6552940 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5552038					
ACCESSION	Bm807097					
VERSION	Bm807097.1	GI:19123920				
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/					
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: gsabbs-remail.nih.gov Tissue Procurement: Lou Staudt CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINT at: http://image.jnl.gov plate: LLM12266 row: 1 column: 23 High quality sequence stop: 104. Location/Qualifiers					
FEATURES						
source	1..1362	/organism="Homo sapiens"				
		/mol_type="mRNA"				
		/db_xref="taxon:9606"				
		/clone="IMAGE:5552038"				
		/tissue_type="lymphoma, cell line"				
		/lab_host="DH10B (phage-resistant)"				
		/clone_id="NH MGC 85"				
		/note="Organ: lymph Vector: PCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed; full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."				
ORIGIN						
Query Match	79.6%;	Score 40.6;	DB 12;	Length 1362;		
Best Local Similarity	91.5%;	Pred. No. 78;				
Matches	43;	Conservative	0;	Mismatches	4; Indels 0; Gaps 0;	
Oy	1	GAGGATGAACCTGAAGAGAGAAGAGAGAGAGAGAGAGA	47			
Db	47	GAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	93			
RESULT 17						
LOCUS	Bb852469	453 bp	mRNA	linear	EST 26-NOV-2001	
DEFINITION	Bb852469 RIKEN full-length enriched, B16 F10Y cells Mus musculus					
ACCESSION	Bb852469					
VERSION	Bb852469.1	GI:17093923				
KEYWORDS	EST.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					

REFERENCE	TITLE	JOURNAL	COMMENT
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 453)			
Authors			
Akimura, T., Arikawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayasuna, N., Hiramoto, K., Hirooka, T., Hirozane, T., Imetani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toyota, T., Watanishi, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.			
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)			
Unpublished (2001)			
Contact: Yoshihide Hayashizaki			
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute			
The Institute of Physical and Chemical Research (RIKEN)			
1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan			
Tel: 81-45-503-9222			
Fax: 81-45-503-9216			
Email: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/			
Carninci, P., Shibata, Y., Hayatani, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.			
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)			
Wagci, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.			
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichipillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)			
Kono, H., Fukushima, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.			
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)			
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.			
e mouse tissues.			
FEATURES			
source			
Location/Qualifiers			
1..453			
/organism="Mus musculus"			
/mol_type="mRNA"			
/strain="C57BL/6J"			
/db_xref="taxon:10090"			
/clone="G370007X15"			
/cell_type="B16 F10Y cells"			
/clone_id="RIKEN full-length enriched, B16 F10Y cells"			
ORIGIN			
Query Match			
Best Local Similarity 79.2%; Score 40.4; DB 10; Length 453;			
Matches 44; Conservativity 0; Mismatches 6; Indels 0; Gaps 0;			
1 GAGGATGAACCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 50			
75 GAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 124			
RESULT 18			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
EST.			
Mus musculus (house mouse)			

AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 553)
Heil, O., Ebert, L., Neubert, P., Peters, M., Radelof, U., Schneider, D. and Korn, B.

TITLE
Mouse Unigeneset - RZPD2

JOURNAL
Unpublished (2003)

COMMENT
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE998J204714.
RZPDLib; I.M.A.G.E. cDNA Clone Collection;
Mouse Unigeneset - RZPD2 (RZPDLib No.981)
http://www.rzpd.de/clonecards/cgi-bin/showLib.pl.cgi?responseLibNo=981
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

FEATURES
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
sugf, primer sequence: CTTCTGCTCTTAAAGCTGCG.
Location/Qualifiers
1..553
/organism="Mus musculus"
/mol_type="cDNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE998J204714 ; IMAGE:1922035"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse kidney mklta"
/note="Organ: kidney; Vector: pME185-FL3; Site_1: DraIII (CACTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer
[ATGCGACCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor (TGTGGCTTACTG), digested and cloned into distinct DraIII sites of the pME185-FL3 vector (5' site CACTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTTAAAGCTGCG and 3' end primer CGACCTGACGCTCGACACA."

ORIGIN

Query Match 79.2%; Score 40.4; DB 13; Length 553;
Best Local Similarity 88.0%; Pred. No. 76;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db
1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGT 50
|||||
48 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 97
|||||

RESULT 19
A2208950 786 bp DNA linear GSS 31-AUG-2000
LOCUS SP_0138_A2_C06_T7A Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=138 Col=12 Row=E, genomic survey sequence.
ACCESSION A2208950
VERSION A2208950.1 GI:8422136
KEYWORDS GSS.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 786)

AUTHORS
Cameron, R.A., Mahairas, G., Raat, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Pouska, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and Hood, L.

TITLE
A sea urchin genome project: Sequence scan, virtual map, and additional resources

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)

MEDLINE
20402566
PUBMED 10920195

COMMENT
Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 138 row: E column: 12
Seq primer: 17
Class: BAC ends
High quality sequence stop: 786.
Location/Qualifiers
1..786
/organism="Strongylocentrotus purpuratus"
/mol_type="genomic DNA"
/db_xref="taxon:7668"
/clone="Plate=138 Col=12 Row=E"
/clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: Bacc3.6; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 79.2%; Score 40.4; DB 28; Length 786;
Best Local Similarity 88.0%; Pred. No. 80;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db
1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGT 50
|||||
94 GAGGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 143
|||||

RESULT 20
B2152227 799 bp DNA linear GSS 11-OCT-2002
LOCUS CH230-504N18.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
DEFINITION CH230-504N18, genomic survey sequence.
ACCESSION B2152227
VERSION B2152227.1 GI:23793178
KEYWORDS GSS.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 799)
Zhao, S., Shetty, J., Shatsman, S., Taegaye, G., Geer, K., Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D., Riggs, E., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment Unpublished (1999)
Other GSSs: CH230-504N18.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdj@jngmail.chi.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end

RESULT 23
BH072396
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BH072396 167 bp DNA linear GSS 18-JUL-2001
RPCI-24-257L19, TV RPCI-24 Mus musculus genomic clone
RPCI-24-257L19, genomic survey sequence.
BH072396
GSS: 14891993
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 167)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akirret, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,
Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSs: RPCI-24-257L19.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (<http://www.tigr.org/bacpac/orderingframe.html>). BAC end
plate: http://www.tigr.org/cdb/bac_end/mouse/bac_end_intro.html
Place: 257 row: L column: 19
Seq primer: T7
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..167
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-257L19"
/sex="Male"
/cell_type="Spleen/Brain"
/clone_1lb="RPCI-24"
/note="Vector: pTARBAC1, Site_1: BamHI, Site_2: BamHI;
RPCI-24 Mouse BAC library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamHI sites using MboI partially digested male C57BL/6J
DNA."

ORIGIN

Query Match 78.4%; Score 40; DB 28; Length 167;
Best Local Similarity 89.6%; Pred. No. 78;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAG 48
|||||
50 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 97
|||||

RESULT 24
CA315228 256 bp mRNA linear EST 09-JUL-2003
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

CA315228 256 bp mRNA linear EST 09-JUL-2003
UI-M-FW0-cd1-b-15-0-UI.r1 NIH BMAP_FW0 Mus musculus cDNA clone
IMAGE:6809872 5', mRNA sequence.
CA315228
CA315228.1 GI:24533352
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 256)
NIH-MGC <http://imgc.ncbi.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA library preparation: Dr. M. Bento Soares, University of Iowa
CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/HLN at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
The following repetitive elements were found in this cDNA
sequence: 37-156, >(GGA)n#simple repeat (matched complement)
82-200, >(GAA)n#simple repeat (matched complement) 201-254,
>(GGA)n#simple repeat (matched complement)
Seq primer: pYX-5

FEATURES
source
Location/Qualifiers
1..256
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6809872"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1lb="NIH BMAP FW0"
/note="Organ: Brain; Vector: pYX-Anc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Anc vector. The library tag
sequence located between the Not I site and the polyA tail
is ACCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hsien Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 78.4%; Score 40; DB 14; Length 256;
Best Local Similarity 89.6%; Pred. No. 83;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAG 48
|||||
Db 101 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 54
|||||

RESULT 25
CF897938 330 bp mRNA linear EST 04-NOV-2003
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

CF897938 330 bp mRNA linear EST 04-NOV-2003
A0231H07-5 NIA Mouse Embryonic Germ Cell cDNA library (Long,
subtracted) Mus musculus cDNA clone NIA:A0231H07 IMAGE:30731418 5',
mRNA sequence.
CF897938
CF897938.1 GI:38164987
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 330)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from


```
/lab host="DH108"  
/clone.lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library  
(long)"  
/notes="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is  
a long-transcript enriched cDNA library (Ref. Genome Res.  
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were  
extracted from a pool of four embryos at 7.5-days  
postcoitum. Double-stranded cDNAs were synthesized with an  
Oligo(dT) primer [Invitrogen:  
5'-pGACTAGTCTAGATCGCGAGCGCCCTTTT-3'] from  
7 ug of total RNA, treated with T4 DNA polymerase, and  
purified by ethanol-precipitation. The cDNAs were ligated  
to lone-linker L1-SalI, purified by phenol/chloroform, and  
separated from free linkers by Centricon 100. Then, the  
cDNAs were amplified by long-range high fidelity PCR using  
Ex Tag polymerase (Takara) with a primer Sal4-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes  
and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
The DH10B E. coli host was transformed with the ligation  
mixture by the standard chemical method. The average  
insert size is about 2.2 kb. The library was constructed  
by Yulan Piao (NIA)."
```

ORIGIN

```
Query Match      78.4%; Score 40; DB 14; Length 373;  
Best Local Similarity 89.6%; Pred. No. 87;  
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      1 GAGGATGAAGCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAG 48  
        ||||| ||||| ||||| ||||| ||||| ||||| |||||  
DB      270 GAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 223
```

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Search completed: February 29, 2004, 21:48:03  
Job time : 2176 secs
```

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Query Match 78.4%; Score 40; DB 4; Length 2663;
Best Local Similarity 89.6%; Pred. No. 0.019;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAGATGAAGCTGAAGAGGAGGAAGAGGAGAGGAGAGGAGAG 48
Db 865 GATGACGAAGATGAGAGGAGGAGGAAGAGGAGGAAGAGGAGAG 912

RESULT 3

US-09-702-705-1668
; Sequence 1668, Application US/09702705
; Patent No. 6504010

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane

APPLICANT: Fan, Liqun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C14

CURRENT APPLICATION NUMBER: US/09/702,705

CURRENT FILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 1833

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1668

LENGTH: 636

TYPE: DNA

ORGANISM: Homo sapiens

US-09-702-705-1668

Query Match 75.3%; Score 38.4; DB 4; Length 636;
Best Local Similarity 87.5%; Pred. No. 0.045;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGATGAAGCTGAAGAGGAGGAAGAGGAGAGGAGAGGAGAG 48
Db 571 GAAGATGAAGAGAGGAGGAGGAAGAGGAGGAAGAGGAGAGGAG 618

RESULT 4

US-09-736-457-1668
; Sequence 1668, Application US/09736457
; Patent No. 6509448

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane

APPLICANT: Fan, Liqun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C15

CURRENT APPLICATION NUMBER: US/09/736,457

CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 1864

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1668

LENGTH: 636

TYPE: DNA

ORGANISM: Homo sapiens

US-09-736-457-1668

Query Match 75.3%; Score 38.4; DB 4; Length 636;
Best Local Similarity 87.5%; Pred. No. 0.045;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGATGAAGCTGAAGAGGAGGAAGAGGAGAGGAGAGGAGAG 48
Db 571 GAAGATGAAGAGAGGAGGAGGAAGAGGAGGAAGAGGAGAGGAG 618

RESULT 5

US-09-614-124B-1668
; Sequence 1668, Application US/09614124B
; Patent No. 6630574

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane

APPLICANT: Fan, Liqun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.478C9

CURRENT APPLICATION NUMBER: US/09/614,124B

CURRENT FILING DATE: 2001-07-11

NUMBER OF SEQ ID NOS: 1668

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1668

LENGTH: 636

TYPE: DNA

ORGANISM: Homo sapiens

US-09-614-124B-1668

Query Match 75.3%; Score 38.4; DB 4; Length 636;
Best Local Similarity 87.5%; Pred. No. 0.045;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGATGAAGCTGAAGAGGAGGAAGAGGAGAGGAGAGGAGAG 48
Db 571 GAAGATGAAGAGAGGAGGAGGAAGAGGAGGAAGAGGAGAGGAG 618

RESULT 6

US-09-671-325-1668
; Sequence 1668, Application US/09671325
; Patent No. 6667154

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane

APPLICANT: Fan, Liqun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C12

CURRENT APPLICATION NUMBER: US/09/671,325

CURRENT FILING DATE: 2000-09-26

NUMBER OF SEQ ID NOS: 1825

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1668

LENGTH: 636

TYPE: DNA

ORGANISM: Homo sapiens

US-09-671-325-1668

Query Match 75.3%; Score 38.4; DB 4; Length 636;
Best Local Similarity 87.5%; Pred. No. 0.045;

RESULT 7
US-09-328-111-333

APPLICANT: Steele, Kathleen E.
APPLICANT: Steele, Kathleen E.

FILE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE NUMBER:

LENGTH: 6
TYPE: DNA
ORGANISM:

Query Match	Score	DB	Length
Best Local Similarity	75.3%	3	650

RESULT 8
US-09-220-132-31

;
; GENERAL INFORMATION
; APPLICANT: Shytan,

CURRENT APPLICATION NUMBER: US/09/220,132
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION:

```
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH 1104
```

LENGTH: 1194
TYPE: DNA
ORGANISM: Homo sapiens

Matches	Conservative	Mismatches	Indels	Gaps
41	0	6	0	0

RESULT 9
US-08-860-038-15

ADDRESS: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:

NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
BIRTHDAY: 03-01-1951

TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 15
SEQUENCE

MOLECULE TYPE:	other nucleic acid
DESCRIPTION:	/desc = "Oligonucleotide"

00-860-038-25

[illegible]

ULT 10
08-860-038-16/

RESULT 10
US-08-860-038-16/c
; Sequence 16, Application US/08860038


```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 316
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-702-705-316
```

```
Query Match          72.2%; Score 36.8; DB 4; Length 1633;
Best Local Similarity 85.4%; Pred. No. 0.12; 7; Indels 0; Gaps 0;
Matches 41; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 48
Db 633 GAAAGTGAAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 680
```

```
RESULT 17
US-09-702-705-788
; Sequence 788, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Dartrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 788
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-702-705-788
```

```
Query Match          72.2%; Score 36.8; DB 4; Length 1633;
Best Local Similarity 85.4%; Pred. No. 0.12; 7; Indels 0; Gaps 0;
Matches 41; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 48
Db 633 GAAAGTGAAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 680
```

```
RESULT 18
US-09-736-457-316
; Sequence 316, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Dartrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
```

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 316
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-316
```

```
Query Match          72.2%; Score 36.8; DB 4; Length 1633;
Best Local Similarity 85.4%; Pred. No. 0.12; 7; Indels 0; Gaps 0;
Matches 41; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 48
Db 633 GAAAGTGAAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 680
```

```
RESULT 19
US-09-736-457-788
; Sequence 788, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Dartrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 788
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-788
```

```
Query Match          72.2%; Score 36.8; DB 4; Length 1633;
Best Local Similarity 85.4%; Pred. No. 0.12; 7; Indels 0; Gaps 0;
Matches 41; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 48
Db 633 GAAAGTGAAGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 680
```

```
RESULT 20
US-09-614-124B-316
; Sequence 316, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Dartrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
```


		0 mismatches	7 Indels	0 Gaps	0;
Cy	4 GATGACCTGAAGAGAGAGAGAGAGAGAGAGAGACTGT				
Db	4135 GATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT				51

RESULT 29
US-09-495

APPLICANT:

[illegible]

RESULT 30
US-09-356


```

ORGANISM: Mus sp.
FEATURE:
NAME/KEY: modified_base
LOCATION: (1001)..(1100)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (2123)..(2222)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (3728)..(3827)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (5168)..(5267)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (7481)..(7580)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (8849)..(8948)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (10375)..(10474)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (12270)..(12369)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (13438)..(13537)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (15902)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (15939)..(16038)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (18223)..(18322)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (20974)..(21073)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (24403)..(24502)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (27574)..(27673)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (30892)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (30901)..(31000)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (34443)..(34542)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (38205)..(38304)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (42373)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (42386)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (42393)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (44261)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (44809)..(44908)
OTHER INFORMATION: a, t, c, g, other or unknown

```

```

OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (51380)..(51479)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (56740)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (56765)..(56864)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (62818)..(62917)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (68518)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (68534)..(68633)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (74552)..(74651)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (81446)..(81545)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (88519)..(88618)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (93791)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (93794)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (96565)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (96570)..(96573)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (96579)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (96590)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (96596)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (96602)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (96616)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (96629)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (96633)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (96668)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (96715)..(96814)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (104447)..(104546)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (114521)
OTHER INFORMATION: a, t, c, g, other or unknown

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[illegible]

```

RESULT 11
US-09-728-446-1420/C
; Sequence 1420, Application US/09728446
; Patent No. US20020081668A1
GENERAL INFORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020081668A1e1 Murine Polynucleotide Sequences
; TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
FILE REFERENCE: Lex-0101-USA
CURRENT APPLICATION NUMBER: US/09/728,446
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,270
NUMBER OF SEQ ID NOS: 1461
SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1420
LENGTH: 234
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(234)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-446-1420

```

```

Query Match      78.4%; Score 40; DB 9; Length 234;
Best Local Similarity 89.6%; Pctd. No. 0.013;
Matches: 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0

Oy      1 GAGCATGAAGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 48
Db      .174 GAGGAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 127

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```

RESULT 12
US-09-728-444-124
/ Sequence 124, Application US/09728444
/ Patent No. US20020161207A1
/ GENERAL INFORMATION:
/ APPLICANT: Friedrich, Glenn
/ APPLICANT: Zembrowicz, Brian
/ APPLICANT: Sende, Arthur T.
/ TITLE OF INVENTION: No. US20020161207A1 Murine Polynucleotide Sequences
/ FILE REFERENCE: LEX-0100-USA and Mutant Cells and Mutant Animals Defined Thereby
/ CURRENT APPLICATION NUMBER: US/09/728,444
/ CURRENT FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/166,360
/ FILING DATE: 1999-12-01
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 124
/ LENGTH: 330

```

```

? TYPE: DNA
? ORGANISM: Mus musculus
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (1) ...(330)
? OTHER INFORMATION: n = A,T,C or G
US-09-728-444-124

```

Query, Match	78.4%;	Score 40;	DB 9;	Length 330,
Best Local Similarity	89.6%;	Pred. No. 0.013;		
Matches	43;	Conservative	0.013;	

Oy
Db

1 GAGGATGAACCTGAAGAAGAGAAAGAGAGAGAGAGAAAG 48
|||||
113 GAGCAGCAAGAGAAAGAAAGCGAAGAGCAAGAGCAAGAGAG 160
|||||

Gaps 0

```

RESULT 13
US-10-425-114-10213
; Sequence 10213 Application US/10425114
; Publication NO. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingtong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 10213
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700899387_FLI
US-10-425-114-10213

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Query Match	78.4%;	Score 40;	DB 12;	Length 642;
Best Local Similarity	89.6%;	Pred. No.	0.012;	
Matches	43;	Conservative	0.012;	

Qy	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Dy	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Dy	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Dy	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Dy	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Dy	1	2	3	4	5	6</																																																																																														

RESULT 14
 US-10-161-927-81
 ? Sequence 81, Application US/10161927
 ? Publication No. US20030203582N1
 ? GENERAL INFORMATION:
 ? APPLICANT: Zehmsen, Bryan D.
 ? APPLICANT: Kerkula, Ramesh
 ? APPLICANT: Spytek, Kimberly A.
 ? APPLICANT: Suenoy, Suresh G.
 ? APPLICANT: Miller, Charles E.
 ? APPLICANT: Hyatt, Todd
 ? APPLICANT: Gerlach, Valerie L.
 ? APPLICANT: Baumgartner, Jason C.
 ? APPLICANT: Guo, Xiaojia
 ? APPLICANT: Gangolli, Bepha A.
 ? APPLICANT: Verner, Corine
 ? APPLICANT: Padiguru, Muralidhara
 ? APPLICANT: Li, Li
 ? APPLICANT: Pena, Carol E.A.
 ? APPLICANT: Gorman, Linda
 ? APPLICANT: Anderson, David W.
 ? APPLICANT: Edinger, Shmuel R.

NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 2663
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G1089
US-09-533-029-47

Query Match 78.4%; Score 40; DB 10; Length 2663;
Best Local Similarity 89.6%; Pred. No. 0.012;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 48
DB 865 GATGACGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 912

RESULT 21
US-09-934-455-177
Sequence 177, Application US/09934455
Publication No. US20030121070A1
GENERAL INFORMATION:
APPLICANT: Adam, Luc
APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Keddie, James
APPLICANT: Pilgrim, Marsha
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, Lynne
APPLICANT: Riechmann, Jose Luis
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PatentIn version 3.1
SEQ ID NO 177
LENGTH: 2663
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (31)...(2427)
OTHER INFORMATION: G1089
US-09-934-455-177

Query Match 78.4%; Score 40; DB 10; Length 2663;
Best Local Similarity 89.6%; Pred. No. 0.012;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 48
DB 865 GATGACGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 912

RESULT 21
US-09-934-455-177
Sequence 177, Application US/09934455
Publication No. US20030121070A1
GENERAL INFORMATION:
APPLICANT: Adam, Luc
APPLICANT: Creelman, Robert
APPLICANT: Dubell, Arnold
APPLICANT: Heard, Jacqueline
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Keddie, James
APPLICANT: Pilgrim, Marsha
APPLICANT: Ratcliffe, Oliver
APPLICANT: Reuber, Lynne
APPLICANT: Riechmann, Jose Luis
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
FILE REFERENCE: MBI-0025
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PatentIn version 3.1
SEQ ID NO 177
LENGTH: 2663
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (31)...(2427)
OTHER INFORMATION: G1089
US-09-934-455-177

Query Match 78.4%; Score 40; DB 10; Length 2663;
Best Local Similarity 89.6%; Pred. No. 0.012;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 48
DB 865 GATGACGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 912

RESULT 22
US-10-225-068-65
Sequence 65, Application US/10225068
Publication No. US20030217383A1
GENERAL INFORMATION:
APPLICANT: Mendel Biotechnology, Inc.

APPLICANT: Reuber, T. Lynne
APPLICANT: Riechmann, Jose Luis
APPLICANT: Heard, Jacqueline E.
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Adam, Luc J.
APPLICANT: Dubell, Arnold T.
APPLICANT: Ratcliffe, Oliver
APPLICANT: Pineda, Omaira
APPLICANT: Yu, Guo-Liang
APPLICANT: Brown, Pierre E.
TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
FILE REFERENCE: 514442002040
CURRENT APPLICATION NUMBER: US/10/225,068
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 65
LENGTH: 2663
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (31)...(2427)
US-10-225-068-65

Query Match 78.4%; Score 40; DB 15; Length 2663;
Best Local Similarity 89.6%; Pred. No. 0.012;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 48
DB 865 GATGACGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 912

RESULT 23
US-10-302-267-45
Sequence 45, Application US/10302267
Publication No. US20030229915A1
GENERAL INFORMATION:
APPLICANT: Keddie, James
APPLICANT: Fromm, Michael
APPLICANT: Heard, Jacqueline
APPLICANT: Riechmann, Jose Luis
APPLICANT: Adam, Luc
APPLICANT: Brown, Pierre
APPLICANT: Pineda, Omaira
APPLICANT: Reuber, Lynne
APPLICANT: Zhang, James
APPLICANT: Yu, Guo-Liang
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Samaha, Raymond
APPLICANT: Pilgrim, Marsha
APPLICANT: Creelman, Robert
TITLE OF INVENTION: PLANT GENE SEQUENCES II
FILE REFERENCE: MBI-0007
CURRENT APPLICATION NUMBER: US/10/302,267
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/120,880
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/121,037
PRIOR FILING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: 60/124,278

Query Match 78.4%; Score 40; DB 15; Length 2663;
Best Local Similarity 89.6%; Pred. No. 0.012;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 48
DB 865 GATGACGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 912

RESULT 23
US-10-302-267-45
Sequence 45, Application US/10302267
Publication No. US20030229915A1
GENERAL INFORMATION:
APPLICANT: Keddie, James
APPLICANT: Fromm, Michael
APPLICANT: Heard, Jacqueline
APPLICANT: Riechmann, Jose Luis
APPLICANT: Adam, Luc
APPLICANT: Brown, Pierre
APPLICANT: Pineda, Omaira
APPLICANT: Reuber, Lynne
APPLICANT: Zhang, James
APPLICANT: Yu, Guo-Liang
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Samaha, Raymond
APPLICANT: Pilgrim, Marsha
APPLICANT: Creelman, Robert
TITLE OF INVENTION: PLANT GENE SEQUENCES II
FILE REFERENCE: MBI-0007
CURRENT APPLICATION NUMBER: US/10/302,267
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/120,880
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/121,037
PRIOR FILING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: 60/124,278

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Query Match      78.4%; Score 40; DB 14; Length 4238;
Best Local Similarity 89.6%; Pred. No 0.011;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy      1 GAGCATGAACTCGAAGACGAGGAAGACACGACGAGCAGAAAGC 48
Db      3299 GAGGAGGAAAGAAGAAGAGGAGGAAAGAAAGGAGGAGGAGGAGAG 346

RESULT 26
US-10-128-714-5204
; Sequence S204, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
```


GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 20:07:24 ; Search time 870 Seconds

(without alignments)
2540.799 Million cell updates/sec

Title: US-09-692-077d-2_COPY_880_930

Perfect score: 51

Sequence: 1 gagagtagaagctgaagagga.....aggaaagtgtrgaaccacag 51

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_ey:*
12: gb_ey:*
13: gb_un:*
14: gb_vl:*
15: gb_vl:*
16: em_ba:*
17: em_fun:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_ey:*
28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pin:*
35: em_hcg_rnd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_ey:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	246	10	S6731782
2	51	100.0	828	10	S67316
3	51	100.0	1344	6	AX350490
4	51	100.0	1344	9	AF316895
5	51	100.0	22842	9	AC092603
6	46.2	90.6	1168	4	PV1251176
7	43	84.3	1180	4	LP4505821
8	43	84.3	1197	4	LP4315941
9	41.8	82.0	6904	6	AX344976
10	41.8	82.0	6904	6	AX348497
11	41.6	81.6	885	9	HSA325747
12	41.6	81.6	1030	9	HSA325747
13	41.6	81.6	1353	6	AX350489
14	41.6	81.6	2072	6	AR270618
15	41.6	81.6	2072	9	HUMADRA2RA
16	41.6	81.6	3274	6	AX548756
17	41.6	81.6	9944	9	AF005900
18	41.4	81.2	1180	9	NCO251186
19	41.4	81.2	1218	10	TTA427262
20	39.8	78.0	1179	10	TTA427266
21	38.8	76.1	1347	10	AF332049
22	38.8	76.1	1347	10	AF332050
23	38.8	76.1	1650	10	MUSADRENH
24	38.8	76.1	2319	10	RATADREN
25	38.8	76.1	6268	10	AF366899
26	38.8	76.1	9377	10	MUSADRECA
27	38.8	76.1	83802	10	AL731836
28	38.8	76.1	124474	2	AC126878
29	38.8	76.1	261258	2	AC091365
30	38.8	75.1	276543	2	AC112830
31	38.4	75.3	1639	10	RNA2BRRA
32	38.2	74.9	1173	4	EAT19810
33	38.2	74.9	1180	10	CPD271336
34	38.2	74.9	1188	4	RTU419814
35	38.2	74.9	1198	4	ECAR2B
36	38.2	74.9	1356	4	AY150337
37	37.2	72.9	194614	2	AC113944
38	37	72.5	301817	2	AC095571
39	36.6	71.8	1180	4	HAM251178
40	36.6	71.8	1185	10	ED0427270
41	36.6	71.8	1185	10	ASP427259
42	36.6	71.8	1203	4	TTB315939
43	36.4	71.4	143350	2	AC121509
44	36.4	71.4	241678	2	AC121484
45	36.4	71.4	254400	2	AC106171
46	36.4	71.4	288697	2	AC133236
47	36.4	71.4	289758	2	AC105607
48	36.4	71.0	216505	2	AC095629
49	36.2	71.0	231171	2	AC132695
50	36.2	71.0	1050	4	AY121768
51	36	70.6	1183	4	OCAR2B
52	36	70.6	1183	4	OCY16189
53	36	70.6	1186	4	MSR251185
54	36	70.6	140251	2	AC132091
55	36	70.6	163847	2	AC102410
56	36	70.6	204820	2	AC130635
57	36	70.6	241347	2	AC134133
58	36	70.2	173614	10	AC125122
59	35.8	70.2	182031	2	AC132383
60	35.8	70.2	185005	2	AC132385
61	35.8	70.2	238103	2	AC099140
62	35.6	69.8	194535	2	AC139950
63	35.6	69.8	214342	2	AC103491
64	35.6	69.8	214342	2	AC116220
65	35.6	69.8	218113	2	AC116220

Prod. No. is the number of results predicted by chance to have a

ORGANISM

Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 22842)
Sulston, J.B. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

9847074
2 (bases 1 to 22842)
Martinka, S., Abbott, A., Hawkins, M., Elliott, G. and Doeber, A.
The sequence of Homo sapiens BAC clone RP11-139J6
Unpublished (2001)
3 (bases 1 to 22842)
Waterston, R.H.
Direct Submission
Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 22842)
Waterston, R.H.
Direct Submission
Submitted (20-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 22842)
Waterston, R.H.
Direct Submission
Submitted (23-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 22842)
Waterston, R.H.
Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 20, 2001 this sequence version replaced gi:14916188.

REFERENCE

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

REFERENCE
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MEDLINE
PUBMED

Query Match	84.3%	Score 43;	DB 4;	Length 1180;
Best Local Similarity	90.2%;	Pred. No. 0.014;		
Matches 46;	Conservative			

[illegible]

LOCUS	LP315941	1197 bp	DNA	linear	MM-22-MAY-2002
DEFINITION	Lama pacos partial adra2b gene for alpha 2B adrenergic receptor.				
ACCESSION	AJ315941				
VERSION	AJ315941.1	GI:21212927			
KEYWORDS	adra2b gene; alpha 2B adrenergic receptor.				
SOURCE	Lama pacos (alpaca)				
ORGANISM	Lama pacos				

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS
 Madhanees I to 1197
 Donady, C. J., Teeling, B. E., O'Brien, S. J., Madson, O., Scally, M.,
 and Springer, M. S., Rydén, O. A., Stanhope, M. J., de Jong, W. W.
 Resolution of the early placental mammal radiation using Bayesian
 phylogenetics
 Science 294 (5550), 2348-2351 (2001)
 11608557
 211793200

of Nijmegen, P.O. Box 9101, 6500 HB Nijmegen, NETHERLANDS

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KYRGLF"
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Page 6

Query Match	84.3%	Score 43;	DB 4;	Length 1197;
Best Local Similarity	90.2%;	Pred. No.	0.014;	
Matches 46;	Conservation			

	Indels	Gaps
Oy	1	0
Db	862	912

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DEFINITION	Sequence 47 from Patent WO0200528.		linear
ACCESSION	AX344976		
VERSION	AX344976.1		
KEYWORDS	GI:18492862		

ORGANISM	synthetic construct
1	artificial sequences.

source	location/Qualifiers
FEATURES	
JOURNAL	Epidemiomics AG (DE)
TITLE	Diagnosis of diseases associated with the immune system
Abstract	Patent: WO 020092-A 47 03 -JAN-2002;
Text	Olek, A.; Pleschbrock, C. and Berlin, K.

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Best Local Similarity 95.6%;
Matches 43.0; Pred. No 0 0 0
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	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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SUBMIT	10
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US	
INVENTION	
AX348497	
Sequence 5	6904 bp
from Parent	DNA
WO0202809.	linear
AX348497	
SION	PAT 06-FEB-2002
WORDS	
GI:18614532	

ORGANISM	synthetic construct
REFERENCE	synthetic construct
	artificial sequences

Journal of the American Academy of Child and Adolescent Psychiatry
Volume 41, Number 1, January 2002
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0885-0666/02/040001-05\$10.00
DOI: 10.1097/00004583-200201000-00001
Printed in the United States of America

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/note="Chemically treated com-
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Local Similarity	Score 41.8; DB 6; Length 6904; Pred No. 0.03; Conservative

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|||||
5880 CTGCTTTT|||||

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[illegible]

[illegible]

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SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
REFERENCE       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS         1 (bases 1 to 1030)
                Kuzenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvashna, S.M., Podowski, R.M., Matushkin, Y.G., Grancharandani, A., Muravenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I., Kiselev, L.L., Wasserman, W., Wahlestedt, C., and Zabarovsky, R.R.
TITLE           NCBI flanking sequences: a tool for gene discovery and verification of the human genome
JOURNAL         Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLIDB        22131767
PUBMED         1213698
REFERENCE       2 (bases 1 to 1030)
AUTHORS         Zabarovsky, E.R.
TITLE           Direct Submission
JOURNAL         Submitted (16-MAY-2001) Microbiology and Tumorigenology Centre, Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77, Sweden

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source         1..1030
               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
               /clone="NB1-8185"

ORIGIN
Query Match    81.6%; Score 41.6; DB 9; Length 1030;
Best Local Similarity 91.7%; Pred. No. 0.036;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY             4 GATGAAGCTGAAGAAGAGGAGAGGAGAGGAAAGTGTGAACCCAG 51
              |||||
Db             187 GAAGAAGAGGAGAGGAGAGGAGAGGAGAGGAAAGTGTGAACCCAG 140

RESULT 13
LOCUS          AX350489                      1353 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION     Sequence 1 from Patent WO0179561.
ACCESSION      AX350489
VERSION        AX350489.1 GI:18616091
KEYWORDS
SOURCE
ORGANISM       Homo sapiens (human)
AUTHORS        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS        1 Liggett, S.B. and Small, K.M.
TITLE          Alpha-2 adrenergic receptor polymorphisms
JOURNAL        Patent: WO 0179561-A 1 25-OCT-2001;
                Liggett, Stephen B. (US); Small, Kersten M. (US)

FEATURES
source         1..1353
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               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

ORIGIN
Query Match    81.6%; Score 41.6; DB 6; Length 1353;
Best Local Similarity 91.7%; Pred. No. 0.036;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY             4 GATAAGCTGAAGAAGAGGAGAGGAGAGGAAAGTGTGAACCCAG 51
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Db             892 GAAGAAGAGGAGAGGAGAGGAGAGGAGAGGAAAGTGTGAACCCAG 939

RESULT 14
LOCUS          AR270618                      2072 bp      DNA      linear      PAT 10-APR-2003
DEFINITION     Sequence 1181 from patent US 6500938.
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/product="alpha 2B adrenergic receptor"  
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Query Match	76.1%	Score 38.8	DB 10	Length 2319
Best Local Similarity	86.0%	Pred. No. 0.22		
Matches 43; Conservative	0	Mismatches 7		

RESULT 25	AF366899	6268 bp	DNA	linear	ROD 15-MAY-2001
LOCUS	AF366899				
DEFINITION	Rattus norvegicus alpha2B-adrenergic receptor (Rng) gene, complete				
ACCESSION	AF366899				
VERSION	AF366899.1				
KEYWORDS	GI:14039788				

SOURCE ORGANISM	REFERENCE AUTHORS	JOURNAL TITLE
Rattus norvegicus (Norway rat)	Schack, S., Cussac, D. and Paris, H.	Unpublished
Rattus norvegicus	1 (bases 1 to 6268)	2 (bases 1 to 6268)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromachi; Muridae; Murinae; Rattus.	Cloning and characterization of the rat alpha2B-adrenergic receptor gene promoter	Submitted
	Direct Submission	Submitted (29-MAR-2001)
	U388, INSERM, CHU Rangueil, Toulouse 31403, France	

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source          location/Qualifiers
1. .6268
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/mol_type="genomic DNA"
/strain="Spizigue-Dawley"
/db_xref="taxon:10116"
1. .5989
/gene="Rng"
1. .2407
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2408. .5989
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ORIGIN

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RESULT	26
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LOCUS	
DEFINITION	MUSADRECA
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
Mus musculus	
	9377 bp DNA linear ROD 24-MAY-2002
	Mus musculus alpha-2C2 adrenergic receptor gene, complete cds.
	M94583.2 GI:21166353
	alpha-2 adrenergic receptor.
	Mus musculus

ORGANISM	Mus musculus (house mouse)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 9377)
JOURNAL	Chen, W.M., Chang, A.C., Shie, B.J., Chang, Y.H. and Chang, N.C.
PUBMED	Molecular cloning and characterization of a mouse alpha 2C2
REFERENCE	adrenoceptor subtype gene
AUTHORS	Biochim. Biophys. Acta 1171 (2), 219-223 (1992)
TITLE	93129625
JOURNAL	1336396
PUBMED	2 (bases 1 to 9377)
REFERENCE	Chen, W.M., Chang, A.C., Wang, C.M., Lin, C.C. and Chang, N.C.
AUTHORS	Characterization of the regulatory regions of murine alpha 2C2
TITLE	adrenoceptor subtype gene
JOURNAL	Neurosci. Lett. 210 (1), 33-36 (1996)
PUBMED	96364053
REFERENCE	8762185
AUTHORS	3 (bases 1 to 9377)
TITLE	Chang, A.C.
JOURNAL	Direct Submission
PUBMED	Submitted (27-APR-1993) Neuroscience, National Yang-Ming
REFERENCE	University, 155, sec. II, Li-Noon St., Taipei, Taiwan 112, Rep. of
AUTHORS	China
TITLE	4 (bases 1 to 9377)
JOURNAL	Chang, A.C.
PUBMED	Direct Submission
REFERENCE	Submitted (24-MAY-2002) Neuroscience, National Yang-Ming
AUTHORS	University, 155, sec. II, Li-Noon St., Taipei, Taiwan 112, Rep. of
TITLE	China
JOURNAL	Sequence update by submitter

Baylor Plaza, Houston, TX 77030, USA
 On Nov 15, 2002 this sequence version replaced gi:23907627.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu>
Contact: hgsc-help@bcm.tmc.edu
Project Information
Center project name: G2CB
Center clone name: CH230-263M16
Summary Statistics
Assembly program: BWA

Consensus quality:	114750 bases at least Q4
Consensus quality:	115674 bases at least Q30
Consensus quality:	116260 bases at least Q20
Estimated insert size:	117568; sum-of-consensus

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Gebnark_draft_data.htm
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

FEATURES
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RESULT	29
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DEFINITION	Rattus norvegicus clone CH230-1A10, *** SEQUENCING IN PROGRESS ***,
ACCESSION	AC091365
VERSION	AC091365.5
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus

REFERENCE
AUTHORS
1 (bases 1 to 261258)
Muzny, D.M., Adams C
sciarognathi; Muridae; Murinae;

Alsbrooks, S. L., Ametung, C., Aido-Ondola, B., Ali-osman, F. R., Allen, C.,
Barberis, J., Benton, J., Bhat, J., Bimague, K., Blankenhorn, M., Banks, T.,
Bouck, J., Bowse, S., Brileva, M., Brown, E., Brown, M., Bryant, D.,
Buhay, C., Burch, P., Burkett, C., Buttrill, K. L., Byrd, M., N.C.,
Carroll, T. F., Carter, M., Cavazos, S. R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowhry, I., Christopoulos, C.,
Cleveland, C. D., Cox, C., Cway, M. D., Dathorne, S. R., David, R.,
Devalla, M. L., Davis, C., Coyle, M. D., Dathorne, S. R., David, R.,
Deane, K. R., Delgado, O., Denn, A. L., Ding, Y., Dinh, H. H.,
Douthwaite, C. J., Draper, H., Dugan-Rocha, S., Durbin, K. J.,
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Massey, E., Mawhney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M.,
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 Scherer, S., Scott, G., Shen, H., Shoostrati, N., Sibson, I.,
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 Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
 Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
 Wu, C., Wu, Y., Wu, Y. P., Zhou, J., Zorrilla, S., Nelson, D.,
 Weinstein, G. and Gibbs, R.
 Direct Submission
 2 (bases 1 to 261258)
 Unpublished
 2 (bases 1 to 261258)
 Worley, K.C.
 Direct Submission
 Submitted (18-APR-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 261258)
 Worley, K.C.
 Direct Submission
 Submitted (10-OCT-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Oct 10, 2002 this sequence version replaced gi:21953942.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/atl/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: TUEV
 Center clone name: CH230-1A10
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 190889 bases at least Q40
 Consensus quality: 198612 bases at least Q30
 Consensus quality: 203158 bases at least Q20
 Estimated insert size: 183633; sum-of-contigs estimation
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_dirfic_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 14 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 4484: contig of 4484 bp in length
 * 4485: gap of unknown length
 * 4585 15356: contig of 10772 bp in length
 * 15357 15456: gap of unknown length

	*	15457	18159	contig of 2703 bp in length
	*	18160	18259	gap of unknown length
	*	18260	118926	contig of 100667 bp in length
	*	118927	119026	gap of unknown length
	*	119027	242237	contig of 123211 bp in length
	*	242238	242337	gap of unknown length
	*	242338	243506	contig of 1169 bp in length
	*	243507	243605	gap of unknown length
	*	243607	245290	contig of 1684 bp in length
	*	245291	245390	gap of unknown length
	*	245391	246466	contig of 1076 bp in length
	*	246467	246566	gap of unknown length
	*	246567	247814	contig of 1248 bp in length
	*	247815	247914	gap of unknown length
	*	247915	249088	contig of 1144 bp in length
	*	249059	249158	gap of unknown length
	*	249159	250644	contig of 1486 bp in length
	*	250645	252774	gap of unknown length
	*	252779	253278	contig of 1534 bp in length
	*	253279	253661	gap of unknown length
	*	253662	253761	contig of 1283 bp in length
	*	253762	261258	gap of unknown length
	*	261258	261258	contig of 7497 bp in length
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				/db_xref="taxon:10116"
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				clone_end:Sp6
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				clone_end:Sp6
				clone_end:EcORI
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				complement(99888..99662)
				/note="clone_boundary
				clone_end:T7
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				end_sequence:BH273948"
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				end_sequence:BH273948"
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				clone_end:T7
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				end_sequence:BH273948"
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				end_sequence:BH273948"
				complement(99327..99667)
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				clone_end:T7
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				end_sequence:BH273948"
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				clone_end:T7
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				end_sequence:BH273948"
				complement(99327..99667)
				/note="clone_boundary
				clone_end:T7
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				clone_end:T7
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				/note="clone_boundary
				clone_end:T7
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, Mon Mar 1 10:03:55 2004

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                  /note="wgs_end_extension
                  clone_end:Sp6"
ORIGIN
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ORIGIN

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Beat Local Similarity	86.0%	Pred. No. 0.19		
Matches 43	Conservative 0	Mismatches 7	Indels 0	Gaps 0

QY 1 GAGGATGAGCTGAAGAAGGAGGAGGAGGAAAGTGTGAACCCCA 50
 |||||
Db 110424 GAGGAGGAGATGAAGAGCATGAGAGGAAGGTGGAAAGATTGAACCCA 110473
 |||||

Search completed: February 29, 2004, 22:17:40
Job time : 891 secs

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[illegible]

DT	04-JUN-2001	(first entry)
XX		
DE	Human	Human alpha2B-adrenoceptor (alpha2B-AR) variant gene.
KW	Human;	cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
KW	glutamic acid repeat;	intracellular loop; chromosome 2; catecholamine;
KW	norepinephrine; ephedrine;	therapy; vascular contraction; variant;
KW	coronary artery;	coronary heart disease; CHD; chronic angina pectoris;
KW	acute myocardial infarction;	AMI; Prinzmetal's variant; ds.
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	1..1344
FT		/*tag= a
FT		/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
FT		variant protein"
PN	WO200129082-A1.	
XX		
PD	26-APR-2001.	
XX		
PF	20-OCT-2000; 2000WO-FI000913.	
XX		
PR	22-OCT-1999; 99US-00422985.	
XX		
PA	(JUVV-) JUVANTIA PHARMA LTD OY.	
PI	Snäpär A, Heinoonen P, Alhopuro P, Karvonen M, Koulu M, Pesonen U;	
PI	Scheinin M, Salonen JT, Tuomahen T, Lakka TA, Nyyssönen K;	
PI	Salonen R, Kaunonen J, Valkonen V;	
DR	WP1; 2001-300318/31.	
DR	P-PSDB; JAE00989.	
XX		
PT	New DNA molecule encoding variant specific adrenoceptor protein with	
PT	deletion of specific amino acids located in the third intracellular loop	
PT	of the polypeptide, for treating vascular contraction of coronary	
PT	arteries.	
XX		
PS	Claim 3; Page 24-26; 37pp; English.	
XX		
CC	The present sequence is a gene encoding human alpha2B-adrenoceptor	
CC	(alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat	
CC	element (amino acids 298-309) of 12 glutamates, in an acidic stretch of	
CC	18 amino acids (amino acids 294-311), located in the third intracellular	
CC	loop of the receptor polypeptide. The variant is obtained by deletion of	
CC	three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR	
CC	gene is located on chromosome 2. Alpha2-AR mediate many of the	
CC	physiological effects of the catecholamines, norepinephrine and	
CC	epinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating	
CC	a mammal suffering from vascular contraction of coronary arteries and a	
CC	disease involving vascular contraction of coronary arteries which is	
CC	clinically expressed as coronary heart disease (CHD), unstable chronic	
CC	angina pectoris which is clinically expressed as Prinzmetal's variant	
CC	form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in	
CC	gene therapy	
XX		
SQ	Sequence 1344 BP; 219 A; 459 C; 400 G; 266 T; 0 U; 0 Other;	
	Query Match	93.7%; Score 47.8; DB 5; Length 1344;
	Best Local Similarity	96.1%; Pred. No. 0.00057;
	Matches 49; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
OY	1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAAAGCTGTAACCCGAG 51	
DB	880 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGCTGTAACCCGAG 930	
RESULT 4		
AAAD4388		
ID	AAAD4388 standard; DNA; 1344 BP.	

PA (EPIC-) EPIDEMIOLOGY AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI, 2002-154759/20.
XX
PT Novel nucleic acid useful for diagnosis and therapy of behavioral
PT disorder, neurological disorder and cancer, comprises a sequence of a
PT segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
PT gene.
XX
PS Claim 1; Page 40-44; 190pp; English.
XX
CC The invention relates to nucleic acids comprising a segment of chemically
CC pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also
CC relates to oligonucleotides or peptide nucleic acid (PNA) oligomers
CC useful for detecting cytosine methylations. The pretreated DNA is useful
CC for the diagnosis or therapy of behavioural disorders, neurological
CC disorders and cancer, in particular major depressive disorder, Tourette's
CC syndrome, schizophrenia, psychiatric and neurological disorders, smoking,
CC drug abuse, alcoholism, personality traits, compulsive gambling, human
CC immunodeficiency virus dementia, migraine, behaviour in schizophrenia
CC and schizoaffective patients, and suicidal behaviour in patients with
CC schizophrenia. The nucleic acid is useful for detecting the methylation
CC state of all CpG dinucleotides and/or single nucleotide polymorphisms
CC (SNPs). The present sequence is human chemically treated genomic DNA
XX
SQ Sequence 6904 BP; 1244 A; 314 C; 2303 G; 3042 T; 0 U; 1 Other;
XX
Query Match 82.0%; Score 41.8; DB 6; Length 6904;
Best Local Similarity 95.6%; Pred. No. 0.025;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGA 45
|||||
DB 5880 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGA 5924
|||||
RESULT 7
AA199905
ID AA199905 standard; DNA; 1353 BP.
XX
AC AA199905;
XX
DT 18-FEB-2002 (first entry)
XX
DE Human alpha-2BAR third intracellular loop encoding DNA.
XX
KW Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
KW polymorphic site; allelic variant; cardiovascular disease;
KW central nervous system disease; adenylyl cyclase; MAP kinase activity;
KW phosphorylation; inositol phosphate; alpha-2BAR;
KW GenBank Accession AF009500; chromosome 2; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1353
FT /tag= a
FT /product= "alpha-2BAR"
FT /note= "sequence includes a 9 nucleotide polymorphic site
FT at nucleotides 901-909 absent in the alpha-2BAR variant
FT (AA199906)"
XX
PP WO200179561-A2.
XX
PN 25-OCT-2001.
XX
PD 17-APR-2001; 2001WO-US012575.
XX
PR 17-APR-2000; 2000US-00551744.
PR 10-AUG-2000; 2000US-00636259.
PR 19-OCT-2000; 2000US-00692077.

XX
XX (LIGG/) LIGGETT S B.
PA (SMAL/) SMALL K M.
XX
XX Liggett SB, Small KM;
XX
DR WPI; 2001-611728/70.
XX
PT P-RSDB; AAM52117.
XX
PT Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for
PT determining whether an individual is at increased risk of developing a
PT disease associated with the corresponding receptor comprises detecting a
PT polymorphic site.
XX
PS Claim 4; Page 144; 163pp; English.
XX
CC The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic
CC receptor gene (I)-(III) by detecting a polymorphic site, comprising: (a)
CC obtaining a sample having a polynucleotide encoding an alpha-2B, alpha2A
CC or alpha2C or fragment or complement of; and (b) detecting a polymorphic
CC site comprising nucleotide positions 901-909 of (I), a site comprising
CC cytosine or guanine at position 753 of (II) or a site comprising (A)
CC (999GCG999GCG) or (B) (999GCG999GCG) at positions 961-972 of (III). The
CC method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor
CC gene and further used to determine whether an individual is at increased
CC risk of developing a disease associated with alpha2B, alpha2A or alpha2,
CC comprising detecting a polymorphic site which correlate to disease
CC selected from cardiovascular disease, central nervous system disease and
CC combinations of these. In addition, the technique may be used to predict
CC an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g.
CC epinephrine, norepinephrine, clonidine, oxymetazoline, guanabenz,
CC UK14304, BHT931 and combinations of these) or antagonist (e.g. yohimbine,
CC prazosin, ARC 239, rauwolfscine, idazoxan, tolazoline, phentolamine and
CC combinations of these) by detecting the polymorphic site and correlating
CC the site to a predetermined response (where the response is correlated to
CC adenylyl cyclase, MAP kinase activity, phosphorylation or inositol
CC phosphate levels). The present sequence is that of the third
CC intracellular loop of the human alpha-2BAR (GenBank Accession AF009500);
CC the sequence includes a 9 nucleotide polymorphic site at nucleotides 901-
CC 909, absent in the alpha-2BAR variant (AA199906)
XX
SQ Sequence 1353 BP; 224 A; 458 C; 405 G; 266 T; 0 U; 0 Other;
XX
Query Match 81.6%; Score 41.6; DB 4; Length 1353;
Best Local Similarity 91.7%; Pred. No. 0.026;
Matches 44; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
QY 4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGAACCCGAG 51
|||||
DB 892 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGAACCCGAG 939
|||||
RESULT 8
AAD04762
ID AAD04762 standard; DNA; 1353 BP.
XX
AC AAD04762;
XX
DT 04-JUL-2001 (first entry)
XX
DE Human alpha2B-adrenoceptor (alpha2B-AR) gene.
XX
KW Human; cardiac; gene therapy; alpha2B-adrenoceptor; alpha2B-AR;
KW glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
KW norepinephrine; epinephrine; therapy; vascular contraction;
KW coronary artery; coronary heart disease; CHD; chronic angina pectoris;
KW acute myocardial infarction; AMI; Prinzmetal's variant; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1353
FT /tag= a

00266617-A1.

P-PSDB; AAR14149.

Isolated DNA encoding human adrenergic receptor - for detecting nucleic

DB	572	GAAGATGATGATGAAGAGAGAGAGAGAGAAAGAAATGTG	614
RESULT 21			
ABN76609			
ID	ABN76609	standard; cDNA; 392 BP.	
AC			
XX	ABN76609;		
XX			
DT	08-JUL-2002	(first entry)	
XX			
DE	Human ORF1556 cDNA, SEQ ID NO:3111.		
XX			
KM	Human; ORF; open reading frame; ORFX; drug screening; diagnosis;		
KM	disease monitoring; cytokine; cell proliferation; cell differentiation;		
KM	immune modulation; haemotopoiesis regulation; tissue growth;		
KM	angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;		
KM	chromolytic; tumour inhibition; bodily characteristics; fertility;		
KM	behaviour; cancer; proliferative disorder; neurological disorder;		
KM	cardiovascular disease; immune system disorder; organ transplantation;		
KM	tissue growth disorder; tissue regeneration disorder; diabetes mellitus;		
KM	hypothyroidism; cholesterol ester storage disease; infection; vulnerability;		
KM	vasotrophic; antiporiatic; antidiabetic; cytosatic; neotopic;		
KM	neuroprotective; antithrombotic; anticoagulant; thrombolytic;		
KM	cardiac; hypotensive; antihypoid; antiinflammatory; immunomodulator;		
KM	dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	MO20190366-A2.		
PD			
XX	29-NOV-2001.		
XX			
PF	24-MAY-2001; 2001WO-US017076.		
XX			
PR	24-MAY-2000; 2000US-0206690P.		
XX			
FA	(CDRA-) CDRA GEN CORP.		
XX			
PI	Leach MD, Shinkets RA;		
DR	WPI; 2002-106200/14.		
XX	P-PSDB; ABP32583.		
PT			
PT	Novel human polypeptides and polynucleotides useful for diagnosing,		
PT	preventing and treating cardiovascular disease, neurodegenerative,		
PT	hyperproliferative disorders and disorders related to organ		
PT	transplantation.		
XX			
XX	Claim 1; Page 1036; 2508BP; English.		
XX			
CC	Sequences ABP11028-ABP35561 represent 4534 novel human proteins		
CC	designated ORF (open reading frame) 1-4534, and sequences ABN75054-		
CC	ABN79587 represent cDNAs encoding them. The invention also encompasses		
CC	polypeptides at least 80% identical to the ORF1-ORF4534 (collectively		
CC	referred to as ORFX) proteins, polynucleotides at least 85% identical to		
CC	the ORFX nucleic acid sequences, vectors and host cells comprising ORFX		
CC	polynucleotides, the recombinant production of ORFX proteins, antibodies		
CC	specific for ORFX proteins, methods of detecting ORFX polynucleotides and		
CC	polypeptides, methods of screening for modulators of ORFX expression or		
CC	activity, and methods of screening individuals for a predisposition to an		
CC	ORFX-associated disorder. The ORFX proteins of the invention have a wide		
CC	range of biological activities, such as cytokine, cell proliferation,		
CC	cell differentiation, immune modulation, haematopoiesis regulation,		
CC	tissue growth, angiogenesis, activin or inhibin activity, chemotactic/		
CC	chemokinetic activity, haemostatic activity, thrombolytic activity,		
CC	receptor/ligand, antiinflammatory activity, tumour inhibition activity,		
CC	and antineoplastic activity, and may also be involved in the determination		
CC	of bodily characteristics, fertility and behaviour. ORFX proteins,		
CC	nucleic acids and antibodies may be used in the treatment of cancers,		
CC	other proliferative disorders such as psoriasis and benign tumours,		
CC	neurological disorders such as epilepsy and Alzheimer's disease,		
CC	cardiovascular diseases, immune system disorders, disorders related to		

CC	organ transplantation, disorders of tissue growth and regeneration, este
CC	diseases such as diabetes mellitus, hypothyroidism, and cholesterol
CC	storage disease, and infectious diseases caused by viral, bacterial,
CC	fungal and other pathogens. ORFX nucleic acids may also be used as a
CC	source of primers and probes, in the detection of ORFX genomic sequences
CC	or transcripts, in the identification and cloning of homologous
CC	sequences, in genetic diagnosis, and in forensic biology. The ORFX
CC	nucleic acids may additionally be used to produce transgenic animals
CC	which may be useful for studying the function and/or activity of ORFX
CC	protein, and in drug screening. The ORFX proteins may also be used as
CC	immunogens to generate specific antibodies, which are useful in the
CC	diagnosis, treatment and monitoring of ORFX-associated diseases
XX	
SQ	Sequence 392 BP; 116 A; 64 C; 112 G; 100 T; 0 U; 0 Other;
Query Match	67.5%; Score 34.4; DB 6; Length 392;
Best Local Similarity	86.4%; Pred. No. 2.1;
Matches 38; Conservative	0; Mismatches 6; Indels 0; Gaps
Dn	
Oy	1 GAGGATTAACCTGAAGAGCGAGCGAGCGAGCAAGAATGTGCA 44
Dd	85 GAAGTGTAGGAGAAAGAGGAGGAGGAGGAGAGGAGAGGAGA 128
RESULT 22	
AAV25477	
ID	AAV25477 standard; cDNA; 5000 BP.
XX	
AC	AAV25477;
XX	
DT	06-AUG-1998 (first entry)
XX	
DE	Rat sulphonylurea receptor SUR2 encoding cDNA.
XX	
KW	Rat; sulphonylurea receptor; SUR2; hypertension; ischaemia;
KW	potaesium channel disease; ss.
OS	Rattus sp.
XX	
FH	Key Location/Qualifiers
FT	CDS 271..4908
FT	/tag= "a"
FT	/product= "SUR2"
FT	/note= "sulphonylurea receptor"
FN	JPI0052275-A.
XX	
PD	24-FEB-1998.
XX	
PF	09-AUG-1996; 96JP-00227552.
XX	
PR	09-AUG-1996; 96JP-00227552.
XX	
PA	(KIYO/) KIYONO S.
PA	(NICH-) JAPAN CHEM RES CO LTD.
DR	WI: 1998-200632/18.
DR	P-PSDB; AAW53602.
XX	
PT	New sulphonyl-urea receptor protein - useful for, e.g. diagnosis and
FT	treatment of potaesium channel diseases such as ischaemia.
XX	
PS	Claim 2; Fig 7-11; 19pp; Japanese.
XX	
CC	The present sequence encodes a new sulphonylurea receptor (SUR2) protein
CC	isolated from a rat brain cDNA library. The sequence can be derived from
CC	animals such as human or rat. Products of SUR2 can be used for diagnosis
CC	and treatment of potaesium channel diseases, e.g. hypertension and
CC	ischaemia
XX	
SQ	Sequence 5000 BP; 1238 A; 1287 C; 1243 G; 1232 T; 0 U; 0 Other;
Query Match	67.5%; Score 34.4; DB 2; Length 5000;

CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.

XX SQ Sequence 6628 BP, 1740 A; 1656 C; 1539 G; 1692 T; 0 U; 1 Other;

Query Match 67.5%; Score 34.4; DB 9; Length 6628;
Best Local Similarity 86.4%; Pred. No. 2.5;
Matches 38; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGTGTGA 44
|||||
DB 3109 GAGGATGAAGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGCA 3152

RESULT 25

ADBS2677 standard; DNA; 6628 BP.

AC ADBS2677;

DT 04-DEC-2003 (first entry)

DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3219.

XX toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
XX toxicity marker; toxicity progression; drug screening;
XX primary rat hepatocyte toxicity modelling; gene; dr.

OS Rattus norvegicus.

XX WO2003065993-A2.

XX 14-AUG-2003.

PF 04-FEB-2003; 2003WO-US003482.

XX 04-FEB-2003; 2002US-035317P.

PR 13-MAR-2002; 2002US-035317P.

PR 08-APR-2002; 2002US-0370248P.

PR 10-APR-2002; 2002US-0371134P.

PR 10-APR-2002; 2002US-0371135P.

PR 11-APR-2002; 2002US-0371413P.

PR 19-APR-2002; 2002US-0373601P.

PR 19-APR-2002; 2002US-0373602P.

PR 22-APR-2002; 2002US-0374139P.

PR 08-MAY-2002; 2002US-0378370P.

PR 09-MAY-2002; 2002US-0378652P.

PR 09-MAY-2002; 2002US-0378653P.

PR 09-JUL-2002; 2002US-0394230P.

PR 09-JUL-2002; 2002US-0394233P.

PR 04-SEP-2002; 2002US-0407688P.

PR 28-JAN-2003; 2003US-0442900P.

XX (GENE-) GENE LOGIC INC.

XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;
XX Elashoff M;
XX MPI; 2003-731472/69.

XX Determining if a compound induces a toxic effect on a tissue or cell, for
XX identifying hepatotoxic compounds, comprises comparing a gene expression
XX profile of a tissue or cell sample to a database of Tox mean and non-Tox
XX mean values.

PS Claim 44; SEQ ID NO 3219; 874pp; English.

XX The present invention describes a method for determining whether a
XX compound induces a toxic effect on a tissue or cell. The method comprises
XX preparing a gene expression profile of a tissue or cell sample exposed to

CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.

CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.

XX SQ Sequence 6628 BP, 1740 A; 1656 C; 1539 G; 1692 T; 0 U; 1 Other;

Query Match 67.5%; Score 34.4; DB 9; Length 6628;
Best Local Similarity 86.4%; Pred. No. 2.5;
Matches 38; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGTGTGA 44
|||||
DB 3109 GAGGATGAAGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGCA 3152

RESULT 26

AAQ29703 standard; DNA; 5125 BP.

AC AAQ29703;

DT 25-MAR-2003 (revised)

DT 17-MAR-1993 (first entry)

XX IRS-1.

XX Insulin receptor substrate-1; IRS-1; probe; vector; transform;

XX IRS-1 metabolism; insulin related disease; sb.

XX Rattus rattus.

XX Key Location/Qualifiers

FT CDS 589..2053

FT /*tag= a

XX MO9213083-A1.

XX 06-AUG-1992.

PF 17-JAN-1992; 92WO-US000437.

PR 18-JAN-1991; 91US-00643982.

XX (JOSL-) JOSLIN DIABETES CENT INC.

XX Kahn CR, White MF, Rothenberg PL;

XX MPI; 1992-365881/44.

DR P-PsDB; AAR28047.

XX Purified nucleic acid encoding Insulin Receptor Substrate - used to
XX prepare IRS-1, for diagnosis and treatment of insulin related diseases
XX and abnormal cellular proliferation.

XX Disclosure, Fig 12; 128pp; English.

PS The sequence given encodes the rat insulin receptor substrate-1 (IRS-1).

XX The IRS-1 was isolated using the probe sequences given in AAQ29701-02.

XX The IRS-1 sequence can be inserted into a vector and used to transform
XX cells to produce IRS-1. The level of IRS-1 metabolism can then be studied
XX and abnormal levels may be seen to be indicative of insulin related
XX disease. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 5125 BP, 1185 A; 1479 C; 1358 G; 1103 T; 0 U; 0 Other;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 14:57:29 : Search time 2149 Seconds
(without alignment)
708.688 Million cell updates/sec

Title: US-09-692-077D-2_COPY_880_930

Perfect score: 51

Sequence: 1 gagagctgaagctggaagagga.....aggaagagctggaaccacag 51

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 150 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gaa_hum:*
18: em_gaa_inv:*
19: em_gaa_pln:*
20: em_gaa_vrt:*
21: em_gaa_fun:*
22: em_gaa_mam:*
23: em_gaa_mus:*
24: em_gaa_pro:*
25: em_gaa_rnd:*
26: em_gaa_phg:*
27: em_gaa_vrt1:*
28: gb_gaa1:*
29: gb_gaa2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41.6	81.6	1353	29	AY416856 Homo sapi
2	40	78.4	1044	13	BQ880026 AGENCOURT
3	38.8	76.1	1347	29	AY416858 Mus muscu
4	38.2	74.9	872	29	ECOA2BAR AL606560 Horse alp

C	5	37.8	74.1	633	9	AL872808	AL872808
C	6	37.8	74.1	634	9	AL852740	AL852740
C	7	37	72.5	642	14	CF360731	CF360731
C	8	37	72.5	787	13	BU748295	BU748295
C	9	36.4	71.4	770	28	B2195097	B2195097
C	10	36.2	71.0	256	14	CA315228	CA315228
C	11	36	70.6	490	9	AA896321	AA896321
C	12	36	70.6	763	14	CB625989	CB625989
C	13	36	70.6	822	14	CB625990	CB625990
C	14	35.4	69.4	365	12	BM659898	BM659898
C	15	35.4	69.4	378	13	BQ294503	BQ294503
C	16	35.4	69.4	399	12	BI961415	BI961415
C	17	35.4	69.4	446	12	BI961033	BI961033
C	18	35.4	69.4	447	9	AL842491	AL842491
C	19	35.4	69.4	496	10	AW760336	AW760336
C	20	35.4	69.4	512	14	CB272922	CB272922
C	21	35.4	69.4	552	14	CF795982	CF795982
C	22	35.4	69.4	556	13	BX669429	BX669429
C	23	35.4	69.4	571	13	BX676418	BX676418
C	24	35.4	69.4	586	9	AI451753	AI451753
C	25	35.4	69.4	608	14	CF367914	CF367914
C	26	35.4	69.4	677	13	CF792336	CF792336
C	27	35.4	69.4	677	13	BY706040	BY706040
C	28	35.4	69.4	823	28	BZ504700	BZ504700
C	29	35.4	69.4	1080	11	AK005900	AK005900
C	30	35.4	69.4	1595	11	AK008242	AK008242
C	31	35	68.6	304	14	CA618111	CA618111
C	32	35	68.6	528	28	A2993348	A2993348
C	33	35	68.6	627	10	BF220068	BF220068
C	34	35	68.6	617	10	AW388194	AW388194
C	35	35	68.2	1009	29	CNS04V62	CNS04V62
C	36	34.8	68.2	464	9	AL791191	AL791191
C	37	34.8	68.2	648	9	AL652867	AL652867
C	38	34.8	68.2	649	9	AL848797	AL848797
C	39	34.8	68.2	861	13	BX736262	BX736262
C	40	34.8	68.2	891	13	BX694066	BX694066
C	41	34.8	68.2	895	13	BX771143	BX771143
C	42	34.8	68.2	899	9	AL970754	AL970754
C	43	34.6	67.8	354	14	CB961043	CB961043
C	44	34.6	67.8	411	14	CD565314	CD565314
C	45	34.6	67.8	516	14	CA567661	CA567661
C	46	34.6	67.8	527	14	BE303747	BE303747
C	47	34.6	67.8	528	9	AA516854	AA516854
C	48	34.6	67.8	560	14	CD544688	CD544688
C	49	34.6	67.8	566	10	BE573037	BE573037
C	50	34.6	67.8	592	14	CF909740	CF909740
C	51	34.6	67.8	598	13	BQ550624	BQ550624
C	52	34.6	67.8	611	14	CA877352	CA877352
C	53	34.6	67.8	618	14	CF908392	CF908392
C	54	34.6	67.8	664	14	CF540205	CF540205
C	55	34.6	67.8	676	14	CB527359	CB527359
C	56	34.6	67.8	689	12	BG871040	BG871040
C	57	34.6	67.8	698	13	BQ769050	BQ769050
C	58	34.6	67.8	706	12	BM963803	BM963803
C	59	34.6	67.8	741	10	BE916440	BE916440
C	60	34.6	67.8	767	12	BI151285	BI151285
C	61	34.6	67.8	889	13	BQ933453	BQ933453
C	62	34.6	67.8	892	13	CK288916	CK288916
C	63	34.6	67.8	919	13	BQ885027	BQ885027
C	64	34.6	67.8	2755	11	AK004698	AK004698
C	65	34.4	67.5	394	14	CF732419	CF732419
C	66	34.4	67.5	478	14	CB731230	CB731230
C	67	34.4	67.5	497	9	AU066373	AU066373
C	68	34.4	67.5	498	10	BF441671	BF441671
C	69	34.4	67.5	537	10	BF077495	BF077495
C	70	34.4	67.5	773	14	CA817872	CA817872
C	71	34.4	67.5	780	12	BI695609	BI695609
C	72	34.4	67.5	804	28	BZ36037	BZ36037
C	73	34.4	67.5	914	14	CF212881	CF212881
C	74	34.4	67.5	1027	12	BM476983	BM476983
C	75	34.4	67.5	1201	9	AL524694	AL524694
C	76	34.2	67.1	501	28	AZ269523	AZ269523
C	77	34.2	67.1	846	29	CNS04HSP	CNS04HSP

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt BioScience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://www.llnl.gov/imagetools>

FEATURES
SOURCE

1. .1044

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6179035"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="lupsk.dorsal root ganglion"
/notes="vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACGATTCGATCGCG-3' and
5'-GACTGATTCGATCGACGCGCGCCCTT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
```

ORIGIN

Query Match	78.4%;	Score 40;	DB 13;	Length 1044;
Best Local Similarity	98.1%;	Pred. No. 23;		
Matches	51;	Conservative	0;	Mismatches 0;
			Indels	1;
			Gaps	1

QY 1 GAGGATGAAGCTGAAGA -GGAGGAGGAGGAGGAAAGTGTGAACCCCAAG 51
Db 417 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAAGTGTGAACCCCAAG 461			

RESULT 3	LOCUS	DEFINITION
AY416858	1347 bp	DNA
AY416858	1347 bp	linear
AY416858	1347 bp	GSS 12-DEC-2001
AY416858	1347 bp	partial sequence,
AY416858	1347 bp	genomic survey sequence.

SOURCE ORGANISM	Mus musculus (house mouse) Mus musculus
-----------------	--

REFERENCE
1 (bases 1 to 1347)

AUTHORS	TITLE	JOURNAL
Clafik, A.G., Glatnowski, S., Nelson, R., Thomas, P., Kojatwal, A., Todd, M.A., Tanenbaum, D.M., Clevello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Satsky, J.J., Adams, M.D. and Carcilli, M.	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios	Science 302 (5652), 1960-1963 (2003)

AUTHORS

TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive

COMMENT	FEATURES	SOURCE
This sequence was made by sequencing genomic exons and ordering them based on alignment.	Location/Qualifiers	1. .1347

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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<!.>1347
locus_tag="Mmu6030"
gene

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ORIGIN

Query Match	76.1%	Score 38.8	DB 29	Length 1347
Best Local Similarity	86.0%	Pred. No. 43		
Matches 43, Conservative	0	Mismatches 7	Indels 0	Gaps 0

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QY      1 GAGATGTAAGCTGAAGAGAGAGAGAGAAGTGTGAACCCA 50
          ||| | | | | | | | | | | | | | | | | | | |
Db      883 GAGAAAGGAGCTGAAGAGATGAAGAGAGAGCTGGAAGATTGAAACCCA 93
```

RESULT 4			
ECAA2BAR			
LOCUS	872 bp	DNA	linear
DEFINITION	Horse alpha2 adrenergic receptor gene fragment probably subtype b, genomic survey sequence.		

SOURCE
Equus caballus (horse)
ORGANISM
Equus caballus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

TITLE	Alpha2 adrenergic receptor gene
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 872)

JOURNAL
Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. UK Email:
biohelp@hgmrc.ac.uk

Source 1. .872

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/organism="Equus caballus"
/mol_type="genomic DNA"
/db_xref="taxon:9796"
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ORIGIN	Score	DB	Length
Query Match	74.9%	29	872
Best Local Similarity	84.3%	55	
Matches	43	0	0
Conservative		8	0
Mismatches			0
Indels			0
Gaps			0

OY 1 GAGGATGAAGCTGAGAGAGGAGAGAGAGAGAGTGTGAACCCAG 51
|||||
Db 592 GAGGAAGAGAGAGAGAGAGAGAGCGGGAGGAAGTGTGAGCTCAG 641

LOCUS	AL872808	633 bp	mRNA	linear	EST 03-DEC-2003
DEFINITION	AL872808	XGC-egg	Silurana	tropicalis	cdna clone TEG106618 5', mRNA
DESCRIPTION	sequence.				

SOURCE ORGANISM	Host	Geographical Location
<i>Silurana tropicalis</i> (western clawed frog)	Human	Guinea
<i>Silurana tropicalis</i>	Human	Guinea

REFERENCE
1 (bases 1 to 633)
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.

TITLE Xanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
COMMENT On Sep 15, 2002 this sequence version replaced gi:22893073
Contact: Taylor R

[illegible][illegible]

1. .256

Program coordinator."

Query Match

ty	83.78;	Score 36.2;	DB 14;	Length 256;
ervative	0;	Mismatch		

AACTGAGAGAGAGCGCCACCAATTTT	Indels	0;	Gaps	0;
----------------------------	--------	----	------	----

[illegible]

490 bp mRNA linear EST 06-APR-1996
Stratagene mouse macrophage (#937306) Mus musculus cDNA
E:1293340 5' similar to gb:156135 Mouse mRNA for
alpha (MOUSE);, mRNA sequence.

GI:3032714

us (house mouse)

Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Eucheria; Rodentia; Sciurognathi; Muridae; Mus.
1 to 490)

Kuehba, D., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Lacy, M., Le, M., Martin, J., Morris, M.,
 Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 HMI Mouse EST Project
 (1996)

Mouse EST Project
University School of Medicine
Park Parkway, Box 8501, St. Louis, MO 63108
6 1800

6 1810
ceest@watson.musrl.edu
is available royalty-free through LNL; contact the
curium (info@nlm.nih.gov) for further information.
-28m13 rev1 ET from Amersham
/ sequence stoc: 148

.490

[illegible]

70.6%;	Score 36;	DB 9;	Length 490;
ty 88.6%;	Pred. No.	1.5e+02;	
ervative			

	0;	Gaps	0;
	0;	Mismatches	5; Indels
AAGCTGAAGAGGAGAGAGAGAGAGAAAGTGTCA			44
AAGGTGAAGAGGAGAGAGAGAGAGAAGACTGTCA			115

3.f OSIIa *Oryza sativa* (indica cultivar-group) CDNA
Ea15013 5', mRNA sequence.

GI:29620978

va (Indica cultivar-group)
va (Indica cultivar-group)
Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryzaceae; Oryza.
763

Arat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Dean, R., Soderlund, C., Wang, R., and Wang, G., Identification of ESTs involved in the interaction between *Arabidopsis thaliana* and *Magnaporthe oryzae* (2003)

Learning
 Economics Institute
 of Arizona
 Sciences West, 448A, P.O. Box 210088,
 Tucson, AZ
 USA
 6 3967

```

1 9288      ://genome.arizona.edu
          aaaa cga cgg cca gtc
          gta aac agc tac gac cat g
          row: 0 column: 13
          gta aaa cga cgg cca gtc.
          ation/Qualifiers
          763

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genium="Oryza sativa (indica cultivar-group)"
1 type="mrna"
altvar="IR36"
xref="caxon:39946"
name="OSIRIA15013"
issue_type="leaf"
v stage="3 week"
host="DH10B"
name_1b="OSIRIA"
ome_vector: plasmidscript II KS +, Site_1: EcoRI, Site_2:
: Lesson Mimic SPL 1"

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70.6%; Score 36; DB 14; Length 763;
88.6%; Pred. No. 1.6e+02;

Matches	39; Conservative	0; Mismatches	5; Indels	0; Gaps	0;
Oy	1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTGA	44			
Db	601 GAGGAAGAAGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGCGA	644			
RESULT 13					
LOCUS	CB625990	822 bp	mRNA	linear	EST 08-APR-2003
DEFINITION	clone OSII15013.r OSII15013.3', mRNA sequence.				
ACCESSION	CB625990				
VERSION	CB625990.1	GI:29620979			
KEYWORDS	EST.				
SOURCE	Oryza sativa (indica cultivar-group)				
ORGANISM	Oryza sativa (indica cultivar-group)				
REFERENCE	Spalholz, D., Dean, R., Soderlund, C., Wang, R. and Wang, G.				
AUTHORS	Jantaeurayrat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., ...				
TITLE	Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA Tel.: 520 626 3967 Fax: 520 621 9288 Email: http://genome.arizona.edu				
FEATURES	PCR Primers FORWARD: gta aaa cga cgg cca gtc BACKWARD: gga aac agc tat gac cat g Plate: 15 row: O column: 13 Seq primer: gga aac agc tat gac cat g. Location/Qualifiers 1..822 /organism="Oryza sativa (indica cultivar-group)" /mol_type="mRNA" /cultivar="IR36" /db_xref="taxon:39946" /clone="OSII15013" /tissue_type="leaf" /dev_stage="3 week" /lab_host="DH10B" /clone_11b="OSII15013" /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; Lesion M1mC SPL 11"				
ORIGIN					
Query Match	70.6%;	Score 36;	DB 14;	Length 822;	
Best Local Similarity	88.6%;	Pred. No. 1.7e+02;			
Matches	39; Conservative	0; Mismatches	5; Indels	0; Gaps	0;
Oy	1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTGA	44			
Db	594 GAGGAAGAAGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGCGA	551			
RESULT 14					
LOCUS	BM659898	365 bp	mRNA	linear	EST 27-FEB-2002
DEFINITION	BU6602768646.R1 CSEGFx138 pig thyroid and parathyroid Sus scrofa				
ACCESSION	BM659898				
VERSION	BM659898.1	GI:18962904			
KEYWORDS	EST.				
SOURCE	Sus scrofa (pig)				
ORGANISM	Sus scrofa				

```

REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
TITLE          Porcine ESTs
JOURNAL        Unpublished (2002)
COMMENT        Contact: David L. Adelson
                Animal Breeding and Genetics
                Texas A&M University
                Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
                USA
                Tel: 9798452616
                Fax: 9798456970
                Email: david.adelson@tamu.edu.

FEATURES
  source
    /organism="Sus scrofa"
    /mol_type="mRNA"
    /db_xref="taxon:9823"
    /clone_lib="GSE0FX18 pig thyroid and parathyroid"
    /note="Organ: thyroid and parathyroid gland; Vector:
    pBluescript SK+; Site 1: NotI; Site 2: EcoRI; sequence 5'
    of the insert (5'-NNN...NNNInsert)
    GCGATTGTGAGCTCCACCGCGTGGCGCGCGCGCTGAG. Sequence 3' of
    the insert (AAGAAATTCGATATCACTTATCGATCCGTCGACCTCGAG.
    non-normalized library, sequenced 3' with M13R primer."

ORIGIN
Query Match      69.4%; Score 35.4; DB 12; Length 365;
Best Local Similarity 86.7%; Pred. No. 2e+02;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy      1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGAGTGTGAA 45
        |||||
        149 GAGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 105

RESULT 15
LOCUS      BQ294503              378 bp      mRNA      linear      EST 15-MAY-2002
DEFINITION Periplaneta americana Lambda Express library Periplaneta
LOCUS      BQ294503              americana cDNA clone 5, mRNA sequence.
ACCESSION  BQ294503
VERSION    BQ294503.1  GI:20803437
KEYWORDS   EST.
SOURCE     Periplaneta americana (American cockroach)
ORGANISM   Periplaneta americana
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
Blattellidae; Periplaneta.
1 (bases 1 to 378)
Zhou Z.W., Liu Z.G. and Gao B.
The construction of Periplaneta americana nymph cDNA library and
19G4 immunology screen
Unpublished (2002)
Contact: Zhou, Z.W.
Immunology Department
Jiang Xi Medical College
106, Bayi Street, Nanchang, Jiangxi, P.R.C.
Tel: 86-0791-6363001
Email: Zhouzhenwen28@hotmail.com.

JOURNAL
COMMENT     Location/Qualifiers
            1. 378
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                /db_xref="taxon:6978"
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                /tissue_type="whole body"
                /dev_stage="nymph"
                /lab_host="E.coli NM522"
                /clone_lib="Periplaneta americana Lambda Express library"
                /note="Vector: Lambda Excell; These sequences were
                screened by cockroach sensitive patients' 19G4 serum "

```


Kiyoshi Kikuchi, Shugo Matabe
Laboratory of Aquatic Molecular Biology and Biotechnology, Graduate
School of Agricultural and Life Sciences, The University of Tokyo,
Bunkyo-ku, Tokyo 108-6639, Japan
Library sequenced by Melody S. Clark and Amanda Thompson MRC Human
Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10
1SB, UK.

Location/Qualifiers
1. .447

Query Match	69.4%	Score 35.4	DB 9	Length 447
Best Local	86.7%	Pred. No. 2e+02		
Matches 39	Conservative 0	Mismatches 6	Indels 0	Gaps 0

QY 1 GAGGATGACCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
 |||||
 Db 215 GAGGATGATGTAAGAGGAGGAGGAGGAGGAAGAAGAGGAGAA 255
 |||||

DEFINITION	LOCUS	AW760336	RESULT 19
81498a06.y1	Gm-cl027	496 bp	mRNA
GENOME SYSTEMS CLONE ID			linear
EST 03-DEC-2001			

ACCESSION	AW760336
VERSION	AW760336.1
	GI:7692223

SOURCE	Glycine max (soybean)
ORGANISM	Glycine max

1 (bases 1 to 496)

AUTHORS	Shoemaker, R., Kelm, P., Vodkin, J., Expeiring, J., Corryell, V., Khanna, A., Bolla, B., Marras, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Treising, B., Allen, M., Bowers, Y., Pearson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
TITLE	Public Soybean EST Project
JOURNAL	Unpublished (1999)
COMMENT	Contact: Shoemaker R/Public Soybean EST Project

oybean EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estowatson.wustl.edu
This clone is available through: Reegen, Invitrogen Corp, 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cu@reegen.com
Insert length: 1134 Std Error: 0.00
High quality sequence. Btop: 424.

Source

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1. .496
/organism="Glycine max"
/mol_type="mRNA"
/db_xref="taxon:3847"
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/lab host="DH10B"
 /clone lib="Gm-cl027"
 /note="Vector: pBluescript II SK(+); Site 1: EcoRI; Site 2:
 XhoI. This cDNA library was constructed from mRNA isolated
 from cotyledons of 3- and 7-day-old Williams seedlings
 which were propagated on paper towels with distilled
 water. The cotyledons were flash-frozen in liquid
 nitrogen, then lyophilized for 72 hours. Unequal amounts
 of mRNA was used for cDNA synthesis. StrataGene's cDNA
 Synthesis Kit (catalog number 200401) was used to
 synthesize the cDNA. First- strand synthesis was
 performed with 5'-methyl dCTP, hence the ligated cDNA was
 hemimethylated. A modification of StrataGene's
 first-strand synthesis primer was used. An anchor
 nucleotide (V=A, C, or G) was added to the 3' end of the
 primer (GAGGAGAGAGAGAGAGACTGTGTCCGAG(7)18) to anchor
 the primer at the 5' end of the poly(A) tract. After
 second- strand synthesis, the cDNA ends were filled in
 with cloned Pfu DNA, ligated to EcoRI adapters and
 subsequently phosphorylated. The XhoI site within the
 first-strand synthesis primer was then restricted by
 digestion with XhoI; all XhoI sites in the cDNA would be
 protected by their hemimethylated status. The cDNA
 constructs were size-fractionated with a 500 bp cutoff,
 using GIBCOBRL Life Technologies' cDNA Size Fractionation
 column. The column eluent was then ligated into
 StrataGene's pBluescript (tm) II XR Predigested vector
 (pBluescript II SK(+)) that has been digested with EcoRI
 and XhoI, and phosphorylated by StrataGene). 97% of the
 white and blue colonies appear to contain recombinant
 plasmids with cDNA inserts, based on size (n=30). This
 library was constructed by Dr. Paul Kelm and Dr. Virginia
 Corryell."

Query March	69.4%	Score 35.4	DB 10	Length 496
Best Local Similarity	84.8%	Pred. No. 2.1e+02		
Matches 39; Conservative	0	Mismatches 7	Indels 0	Gaps 0

QY 1 GAGGATGAGCTGAAGAGAGGAGGAGGAGAGAGTGTGTAAAC 46
Db 365 GAGGATGAGGATATGAGAGGAGGAGGAGGAGATGTGTTATACC 410

RESULT 20

LOCUS	CB272922	512 bp	RNA	linear	EST 24-FEB-2007
DEFINITION	ma6d407.y1 McCarrey Eddy spermatocytes	Mus musculus	cdna	clone	
IMAGE	6446341	5', mRNA sequence.			

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 512)
McCarthy, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Page, D.,
Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M.,
Ritter, E., Tsagarrelshvili, R., Ronko, I., Maguire, L., Kennedy, S.,
Bennett, J., Waterston, R. and Wilson, R.
NIHES Mouse
Unpublished
Contact: McCarthy/Eddy NIHES Mouse

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

Query Match 69.4%; Score 35.4; DB 13; Length 556;
 Best Local Similarity 86.7%; Pred. No. 2.1e+02;
 Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGTGTGAA 45
 |||||
 395 GAGGAGGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 439

RESULT 23
 BX676418 571 bp mRNA linear EST 28-OCT-2003
 LOCUS BX676418 Sus scrofa library (scac) Sus scrofa cDNA clone
 DEFINITION scac00311.e.12 3prtm, mRNA sequence.
 BX676418
 VERSION BX676418.1 GI:38010553
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 1 (bases 1 to 571)
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villegier, S.,
 Soares, M., Bonaldi, F. and Haley, F.
 A Pig Normalised Multi-Tissue cDNA Library
 Unpublished (2003)
 Contact: Tosser-Klopp G
 Genetique Animale
 Institut National de la Recherche Agronomique
 Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
 cedex, FRANCE
 Tel: 33 (0) 5.61.28.51.14
 Fax: 33 (0) 5.61.28.53.08
 Email: tosser@clouise.inra.fr
 Clone distribution: AGENAE Resource centre, Francois PUMI,
 Francois.Plum@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du
 genome (LRBG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,
 FRANCE. +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
 Sequence cleaned of vector, adaptor and repetitions. Contact us
 at bigenae@portjouy.inra.fr to obtain the chromatogram of this
 sequence.
 Plate: 0031, row: e column: 12.
 Location/Qualifiers
 1..571
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="scac00311.e.12"
 /tissue_type="mixed"
 /clone_lib="Sus scrofa library (scac)"
 /note="Vector: pT73D-pac vector; tissues: adipose tissue,
 brain, kidney, liver, muscle, ovary, testis, heart,
 hypochalamus, pancreas, skin, spleen, thymus, placenta,
 pituitary gland, seminal vesicle, small intestine,
 uterus, adrenals, bulbo urethral gland, cerebral trunk,
 epididymis, female gonad, gall-bladder, hippocampus,
 large intestine, male gonad, melanocytes, stomach, udder"

ORIGIN
 Query Match 69.4%; Score 35.4; DB 13; Length 571;
 Best Local Similarity 86.7%; Pred. No. 2.1e+02;
 Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGTGTGAA 45
 |||||
 395 GAGGAGGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 439

RESULT 24
 A1451753 586 bp mRNA linear EST 15-MAR-2000
 LOCUS A1451753/c
 DEFINITION mb16f09.y1 Soares mouse p3NMFI9.5 Mus musculus cDNA clone
 IMAGE:329609 5' similar to TR:Q12804 Q12804 RECEPTIN.;, mRNA

sequence.
 accession A1451753
 version A1451753.1 GI:4306203
 keywords EST.
 source Mus musculus
 organism Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 586)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
 Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R.,
 Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterson, R. and Wilson, R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mousee@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 This read is a RESEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the
 correct orientation)
 MG1:211009
 Seq primer: -40RP from G1bco
 High quality sequence scop: 457
 POLYA=No.
 Location/Qualifiers
 1..586
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:329609"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="PH10B (ampicillin resistant)"
 /clone_lib="Soares mouse p3NMFI9.5"
 /note="Vector: pT73D (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTTCAATCTGAGTGGAGCGGCCGATTTTCTTTTCTTTT 3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M.Fatima Bonaldi. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."

ORIGIN
 Query Match 69.4%; Score 35.4; DB 9; Length 586;
 Best Local Similarity 86.7%; Pred. No. 2.1e+02;
 Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGTGTGAA 45
 |||||
 227 GAGGAGGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGTGA 183

RESULT 25
 CF367914 608 bp mRNA linear EST 25-AUG-2003
 LOCUS CF367914/c
 DEFINITION 852497 MARC 3P1G Sus scrofa cDNA 3', mRNA sequence.
 accession CF367914
 version CF367914.1 GI:34172915
 keywords EST.
 source Sus scrofa (pig)
 organism Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

TITLE

rosidae; eucosidae II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 823)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Frazer, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other GSSs: BOMRX59TF
Contact: Chris Town

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Classes: sheared ends.
Location/Qualifiers
1. 823
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone="BOMRX59"
/clone_1b="BO.1.6.2 KB tot"
/note="Vector: PHOS1; Site 1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHD1 using BstXI linkers"

Ch 69.4%; Score 35.4; DB 28; Length 823;
1 Similarity 86.7%; Pred. No. 2.2e+02;
39; Conservative 0; Mismatches 6; Indels 0; Gaps 0

1 GAGGATGAAGCTCGAAGAGGAGGAGGAGGAGGAGGAAGTGTGA 45
|||||
10 GAGGAGGAGGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGA 84
|||||

AK005900 1080 bp mRNA linear HTC 20-SEP-2001
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:1700012D1 product:similar to CBP1 INTERACTING
CORRESPONDOR CIR [Homo sapiens], full insert sequence.
AK005900.1 GI:12838722
AK005900.1
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komano, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

3
Shibata, K., Itoh, M., Aizawa, K., Nagaoke, S., Sasaki, N., Carninci, P.,
Komano, H., Akiyama, J., Nishi, K., Katsunai, T., Taahiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS

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AUTHORS

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JOURNAL

DB

RESULT 30

AK008242/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

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REFERENCE

Kanagawa 230-0045, Japan (E-mail:genome-res@gsic.riken.go.jp,
URL: <http://genome.gsic.riken.go.jp/>, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (<http://genome.gsic.riken.go.jp/>) for
further details.

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5' GAGAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTNN 3'], cDNA was
prepared by using trihalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. cDNA went
through one round of normalization to Rot = 5.0 and subtraction to
Rot = 20.0. Second strand cDNA was prepared with the primer adapter
of sequence [5'
GAGAGAGAGATTCGAGTTAATTAAATTAATCCCCCCCCCCC 3']. cDNA was cleaved
with XhoI and ScaI. Cloning sites, 5' end: XhoI; 3' end: ScaI.
Host: SOLR.

FEATURES

source

location/Qualifiers

1..1595
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:2010015A19"
/db_xref="MGI:1898921"
/db_xref="taxon:10090"
/clone="2010015A19"
/sex="male"
/issue_type="small intestine"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"

misc_feature

1..1595
/note="similar to CBP1 INTERACTING COREPRESSOR CIR (Homo
sapiens) (SPTRL095367, evidence: FASTY, 77.6%ID,
96.4%length, match=1347)"

ORIGIN

Query Match 69.4%; Score 35.4; DB 11; Length 1595;
Best Local Similarity 86.7%; Pred. No. 2.5e+02;

Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 GAGATGAACTGAGAGAGAGAGAGAGAGAGAGAGAGTGA 45
|||||
Db 922 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAA 878

Search completed: February 29, 2004, 21:48:25
Job time : 2171 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: February 29, 2004, 20:27:29 ; Search time 62.5 Seconds
(without alignments)
452,840 Million cell updates/sec

Title: US-09-692-077D-2_COPY_880_930

Perfect score: 51
Sequence: 1 gagagtagaacgcgaagagga.....aggaaagcgtgaacccag 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/2/ina/5A COMB. seq:*
- 2: /cgn2_6/prodata/2/ina/5B COMB. seq:*
- 3: /cgn2_6/prodata/2/ina/6A COMB. seq:*
- 4: /cgn2_6/prodata/2/ina/6B COMB. seq:*
- 5: /cgn2_6/prodata/2/ina/PCTUS COMB. seq:*
- 6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	41.6	81.6	2072	4 US-09-016-434-1181	Sequence 1181, Ap
2	36.6	71.8	593	4 US-09-691-538A-12	Sequence 12, Appl
3	35	68.6	1820	5 PCT-US94-09752-1	Sequence 1, Appl
4	34.2	67.1	5125	1 US-08-094-948A-4	Sequence 4, Appl
5	34.2	67.1	5125	5 PCT-US96-09319-4	Sequence 4, Appl
6	33	64.7	650	3 US-09-328-111-333	Sequence 333, App
7	32.8	64.3	404	4 US-09-621-976-18769	Sequence 18769, A
8	32.6	63.9	661	4 US-09-894-998A-34	Sequence 34, Appl
9	32.2	63.1	2817	4 US-09-620-312D-1085	Sequence 1085, Ap
10	32.2	63.1	14561	4 US-09-392-714-1	Sequence 1, Appl
11	31.8	62.4	636	4 US-09-702-705-1668	Sequence 1668, Ap
12	31.8	62.4	636	4 US-09-736-457-1668	Sequence 1668, Ap
13	31.8	62.4	636	4 US-09-614-124B-1668	Sequence 1668, Ap
14	31.8	62.4	636	4 US-09-671-325-1668	Sequence 1668, Ap
15	31.6	62.0	258	4 US-09-345-882-21	Sequence 21, Appl
16	31.6	62.0	3211	2 US-08-574-859A-8	Sequence 8, Appl
17	31.6	62.0	3211	3 US-09-357-014-8	Sequence 8, Appl
18	31.6	62.0	3901	3 US-08-574-859A-6	Sequence 6, Appl
19	31.6	62.0	3901	3 US-09-357-014-6	Sequence 6, Appl
20	31.6	62.0	4226	4 US-09-620-312D-480	Sequence 480, App
21	31.6	62.0	6002	4 US-09-345-882-4	Sequence 4, Appl
22	31.6	62.0	162450	4 US-09-345-882-1	Sequence 1, Appl
23	31.4	61.6	2556	4 US-09-817-310-1	Sequence 1, Appl
24	31.2	61.2	129	4 US-09-702-705-309	Sequence 309, App
25	31.2	61.2	129	4 US-09-736-457-309	Sequence 309, App
26	31.2	61.2	129	4 US-09-614-124B-309	Sequence 309, App
27	31.2	61.2	129	4 US-09-671-325-309	Sequence 309, App

C	28	31.2	61.2	129	4	US-09-589-184-309	Sequence 309, App
	29	31.2	61.2	403	4	US-09-621-976-18731	Sequence 18731, A
	30	31.2	61.2	427	4	US-09-621-976-18711	Sequence 18711, A
	31	31.2	61.2	438	4	US-09-702-705-1028	Sequence 1028, Ap
	32	31.2	61.2	438	4	US-09-736-457-1028	Sequence 1028, Ap
	33	31.2	61.2	438	4	US-09-614-124B-1028	Sequence 1028, Ap
	34	31.2	61.2	438	4	US-09-671-325-1028	Sequence 1028, Ap
	35	31.2	61.2	450	4	US-09-621-976-3667	Sequence 3667, Ap
	36	31.2	61.2	452	4	US-09-621-976-3669	Sequence 3669, Ap
	37	31.2	61.2	458	4	US-09-621-976-1227	Sequence 1227, Ap
	38	31.2	61.2	459	4	US-09-621-976-1224	Sequence 1224, Ap
	39	31.2	61.2	464	4	US-09-621-976-1223	Sequence 1223, Ap
	40	31.2	61.2	464	4	US-09-621-976-3665	Sequence 3665, Ap
	41	31.2	61.2	464	4	US-09-621-976-18704	Sequence 18704, A
	42	31.2	61.2	476	4	US-09-621-976-18704	Sequence 18704, A
	43	31.2	61.2	514	4	US-09-621-976-3661	Sequence 3661, Ap
	44	31.2	61.2	521	4	US-09-621-976-18772	Sequence 18772, A
	45	31.2	61.2	686	4	US-09-166-350-9	Sequence 9, Appl
	46	31.2	61.2	1147	4	US-09-016-434-1251	Sequence 1251, Ap
	47	31.2	61.2	1275	1	US-08-552-142A-3	Sequence 3, Appl
	48	31.2	61.2	1275	1	US-08-910-973-3	Sequence 3, Appl
	49	31.2	61.2	1275	1	US-09-499-227-3	Sequence 3, Appl
	50	31.2	61.2	1275	5	PCT-US95-05741-3	Sequence 3, Appl
	51	31.2	61.2	2663	4	US-09-533-029-47	Sequence 47, Appl
C	52	31.2	61.2	2663	4	US-09-533-029-47	Sequence 47, Appl
	53	31.2	61.2	5561	4	US-09-418-710-28	Sequence 28, Appl
	54	31.2	61.2	5573	4	US-09-418-710-30	Sequence 30, Appl
	55	31	60.8	675	1	US-07-807-043B-2	Sequence 2, Appl
	56	31	60.8	675	1	US-08-299-849B-2	Sequence 2, Appl
	57	31	60.8	675	2	US-08-142-368A-2	Sequence 2, Appl
	58	31	60.8	675	4	US-09-312-464-2	Sequence 2, Appl
	59	31	60.8	675	3	US-08-967-727-2	Sequence 2, Appl
	60	31	60.8	675	4	US-09-583-850-2	Sequence 2, Appl
	61	31	60.8	675	4	US-09-579-197-2	Sequence 2, Appl
	62	31	60.8	675	4	US-09-404-026-2	Sequence 2, Appl
	63	31	60.8	675	4	US-09-312-464-2	Sequence 2, Appl
	64	31	60.8	1365	1	US-07-807-043B-4	Sequence 4, Appl
	65	31	60.8	1365	1	US-08-299-849B-4	Sequence 4, Appl
	66	31	60.8	1365	2	US-08-142-368A-4	Sequence 4, Appl
	67	31	60.8	1365	3	US-08-967-727-4	Sequence 4, Appl
	68	31	60.8	1365	3	US-08-037-230D-4	Sequence 4, Appl
	69	31	60.8	1365	4	US-09-583-850-4	Sequence 4, Appl
	70	31	60.8	1365	4	US-09-579-197-4	Sequence 4, Appl
	71	31	60.8	1365	4	US-09-404-026-4	Sequence 4, Appl
	72	31	60.8	1365	4	US-09-312-464-4	Sequence 4, Appl
	73	31	60.8	2184	3	US-08-953-918C-1	Sequence 1, Appl
	74	31	60.8	2184	4	US-08-697-766A-1	Sequence 1, Appl
	75	31	60.8	2518	3	US-09-433-699-3	Sequence 3, Appl
	76	31	60.8	4698	1	US-07-807-043B-5	Sequence 5, Appl
	77	31	60.8	4698	1	US-08-299-849B-5	Sequence 5, Appl
	78	31	60.8	4698	2	US-08-142-368A-5	Sequence 5, Appl
	79	31	60.8	4698	3	US-08-967-727-5	Sequence 5, Appl
	80	31	60.8	4698	3	US-08-037-230D-5	Sequence 5, Appl
	81	31	60.8	4698	4	US-09-583-850-5	Sequence 5, Appl
	82	31	60.8	4698	4	US-09-579-197-5	Sequence 5, Appl
	83	31	60.8	4698	4	US-09-404-026-5	Sequence 5, Appl
	84	31	60.8	4698	4	US-09-312-464-5	Sequence 5, Appl
	85	31	60.8	6114	4	US-09-495-716A-5	Sequence 5, Appl
	86	30.8	60.4	1194	4	US-09-220-132-31	Sequence 31, Appl
	87	30.8	60.4	2120	4	US-09-220-132-31	Sequence 31, Appl
	88	30.8	60.4	2277	4	US-09-149-476-160	Sequence 160, App
C	89	30.8	60.4	2277	4	US-09-310-463-3	Sequence 3, Appl
	90	30.8	60.4	2790	4	US-08-842-248A-3	Sequence 3, Appl
	91	30.8	60.4	2790	3	US-08-985-950-21	Sequence 21, Appl
	92	30.8	60.4	2922	4	US-09-310-463-1	Sequence 1, Appl
	93	30.8	60.4	2922	4	US-08-842-248A-1	Sequence 1, Appl
	94	30.6	60.0	58	3	US-08-860-023-16	Sequence 16, Appl
	95	30.6	60.0	1954	4	US-09-580-923-16	Sequence 16, Appl
	96	30.6	60.0	1954	4	US-08-997-829-3	Sequence 3, Appl
C	97	30.6	60.0	1954	1	US-08-577-403-3	Sequence 3, Appl
	98	30.6	60.0	2520	4	US-09-023-655-917	Sequence 917, App
	99	30.6	60.0	2581	4	US-09-370-838-66	Sequence 66, Appl
	100	30.6	60.0	3164	4	US-09-023-655-816	Sequence 816, App


```

PCT-US94-09752-1
; Sequence 1, Application PC/TUS9409752
; GENERAL INFORMATION:
; APPLICANT: David S. Strayer and Avinash Chander
; TITLE OF INVENTION: Compositions and Methods for
; NUMBER OF INVENTIONS: Targeting Cells and Modulating Pulmonary Surfactant Secretion
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09752
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/176,218
; FILING DATE: December 30, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/114,951
; FILING DATE: August 31, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: JEFF-0042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1820
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; PCT-US94-09752-1
;
Query Match 68.6%; Score 35; DB 5; Length 1820;
Best Local Similarity 88.4%; Pred. No. 0.1;
Matches 38; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
;
Oy 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGAGAGTGTG 43
Db 572 GAAGATGATGATGAAGAGAGAGAGAGAGAGAGAGAGAGATGTG 614
;
RESULT 4
US-08-094-948A-4
; Sequence 4, Application US/08094948A
; Patent No. 5621075
; GENERAL INFORMATION:
; APPLICANT: Kahn, C. Ronald
; APPLICANT: White, Morris F.
; APPLICANT: Rothenberg, Paul Louis
; TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahnive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//08//094,948A
FILING DATE: 21-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,982
FILING DATE: 18-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-013DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5125 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 589..4053
US-08-094-948A-4

Query Match      67.1%; Score 34.2; DB 1; Length 5125;
Best Local Similarity 83.0%; Pred. No. 0.19;
Matches 39; Conservative 0; Mismatches 8; Indels 0; Gaps 0.

Oy      3 GGATGAAGCTGAAAGAGAAGAGAAGAGAAGAAAGTGTGAACCCC 49
Db      53 GGAGAGAGCAGAGAGAGAGAGAAGAGAAGAGAAGAGAAGAACCCC 99

RESULT 5
PCT-US96-09319-4
Sequence 4, Application PC/TUS9609319
GENERAL INFORMATION:
APPLICANT: Kahn, C. Ronald
APPLICANT: White, Morris F.
APPLICANT: Rothenberg, Paul Louis
TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: Lahive & Cockfield
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09319
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/094,948
FILING DATE: 21-JULY-1993
APPLICATION NUMBER: US 07/643,982
FILING DATE: 18-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-013DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

```

ORGANISM: Homo sapiens
US-09-621-976-18769

Base% match:	64.3%	Score 32.8:	DB 4:	Length 404:
Best Local Similarity	84.1%	Pred. No. 0.37:		
Matches 37;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0
1	GAGGATGAACTGTAAGCGAGGAGCGAGCGAGGAGGAGTGTGA	44		

348 GAGGAAGACGTGGGGAGCAGCAGGAGGAGGAGGAGAGAGATGTGA 391

```

RESULT 8
US-09-894-998A-34/c
; Sequence 34, Application US/09894998A
; Patent No. 6537555
; GENERAL INFORMATION:
; APPLICANT: Hosken, Nancy Ann
; APPLICANT: Craig H. Day
; APPLICANT: Davlin C. Dillon
; APPLICANT: McGowan, Patrick
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
; CURRENT APPLICATION NUMBER: US/09/894, 998A
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 661
; TYPE: DNA
; ORGANISM: HSV-2
US-09-894-998A-34

Query Match
Best Local Similarity 63.9%; Score 32.6; DB 4; Length 661;
Matches 35; Conservative 0; Mismatches 4; Indels 0; Gaps 0
1 GAGGATGAAGTGAAGAGCAGCAGCAGCAGCAGGAAG 39
|||
Db 42 GAGGAGCAGCGCGGAGGAGGAGGAGGAGCGGAAAG 4
|||

```

US-09-620-312D-1085
; Sequence 1085, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Asundi, Vinod

APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yuedi

QY
1 GAGGATGAAGCTGAGAGAGAGAGAGAGAAAGTGTGAACCCAG 51
|||||
586 GAGAGAGAAGAGAGAGAGAGAGAGAGATGATTATGACTCAG 636
|||||

[illegible]

Query Match	62.4%	Score 31.8;	DB 4;	Length 636;
Best Local Similarity	76.5%;	Pred. NO. 0.74;		
Matches	39; Conservative	0; Mismatches	12; Indels	0; Gaps
QY	1	GAGGATGAACGTGAAAGACAGCAGCAGCAGCAGCAAGAGTGTGAACCACG	51	
Db	586	GAGCGAAGAAGAACGAGAGCAGCAGCAGCAGCAGCAGCAGCAGTAATGACTCCAG	636	

RESULT 15
 US-09-345-892-21
 : Sequence 21, Application US/09345882
 : Patent No. 6399373
 : GENERAL INFORMATION:
 : APPLICANT: Bouguetelrec, Lydie
 : TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBB-7)
 : TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID
 : FILE REFERENCE: GENSET.031A

```

? CURRENT APPLICATION NUMBER: US/09/345,882
? CURRENT FILING DATE: 1999-06-30
? PRIOR APPLICATION NUMBER: US 60/991,315
? PRIOR FILING DATE: 1998-06-30
? PRIOR APPLICATION NUMBER: US 60/111,909
? PRIOR FILING DATE: 1998-12-10
? NUMBER OF SEQ ID NOS: 140
? SOFTWARE: Patent.pm
? SEQ ID NO 21
? LENGTH: 258
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-345-882-21

```

Query Match	62.0%	Score 31.6;	DB 4;	Length 258;
Best Local Similarity	89.5%	Pred. No. 0.77;		
Matches	34;	Conservative	0.0	Matched

Q7 1 GAGGATGAACCTCGAAGAGAAGAGGAGAGAGAGAAAGA 38
| | | | | | | | | | | | | | | | | | | | | |
D6 32 GATGAAGAAGCAGAAAGAGAGAGAGAGAGAGAGAAAGAAGA 69
| | | | | | | | | | | | | | | | | | | | | |

```

1      RESULT 16
2      US-08-574-959A-8
3      Sequence 8, Application US/00574959A
4      Patent No. 5662224
5      GENERAL INFORMATION:
6      APPLICANT: Jaekyoung Shin, Insl Joung, Ratna K.
7      APPLICANT: and Jack L. Strominger
8      TITLE OF INVENTION: D62 POLYPEPTIDES, RELATED P
9      NUMBER OF SEQUENCES: 22
10     CORRESPONDENCE ADDRESSES:
11     ADDRESSEE: LAHIVE & COCKFIELD
12     STREET: 60 State Street, Suite 510
13     City: Boston
14     STATE: Massachusetts
15     COUNTRY: USA
16     ZIP: 02109-1875
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: Floppy disk
19     COMPUTER: IBM PC compatible
20     OPERATING SYSTEM: PC-DOS/MS-DOS
21     SOFTWARE: PatentIn Release #1.0, Version #1.25
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/08/574,959A
24     FILING DATE: 19-DEC-95
25     ATTORNEY/AGENT INFORMATION:
26     NAME: Mandragoras, Amy E.
27     REGISTRATION NUMBER: 36,207
28     REFERENCE/DOCKET NUMBER: DFN-008
29     TELECOMMUNICATION INFORMATION:
30     TELEPHONE: (617)227-7400
31     TELEFAX: (617)227-5941
32     INFORMATION FOR SEQ ID NO: 8:
33     SEQUENCE CHARACTERISTICS:
34     LENGTH: 3211 base pairs
35     TYPE: nucleic acid
36     STRANDEDNESS: single
37     TOPOLOGY: linear
38     MOLECULE TYPE: DNA
39     FEATURE:
40     NAME/KEY: CDS
41     LOCATION: 439..3157
42     US-08-574-959A-8

```

```
Query Match      62.0%; Score 31.6; DB 2; Length 321;
Best Local Similarity 89.5%; Pred No. 0.96;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps
1 GAGGATGAAGCTGGAAAGCAGAGGAGGAGGAGGAGA 38
|||||
```

Db 2590 GAGGAGAGAGAGAGAGAGAGATGAGAGAGAGAGA 2627

RESULT 17

US-09-357-014-8

Sequence 8, Application US/09357014

Patent No. 6291645

GENERAL INFORMATION:

APPLICANT: Jaekyoon Shin, Insil Joungh, Ratna K. Vadlamudi

and Jack L. Strominger

TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES

AND USUS THEREFOR

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/357,014

FILING DATE: 19-Jul-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/574,959

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 3211 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 439..3157

SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-357-014-8

Query Match

Best Local Similarity 62.0%; Score 31.6; DB 3; Length 3211;

Best Local Similarity 89.5%; Pred. No. 0.96;

Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGA 38

Db 2590 GAGGAGAGAGAGAGAGAGAGATGAGAGAGAGAGA 2627

RESULT 18

US-08-574-959A-6

Sequence 6, Application US/08574959A

Patent No. 5962224

GENERAL INFORMATION:

APPLICANT: Jaekyoon Shin, Insil Joungh, Ratna K. Vadlamudi

and Jack L. Strominger

TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES

AND USUS THEREFOR

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/574,959A

FILING DATE: 19-DEC-95

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 3901 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 439..3847

US-08-574-959A-6

Query Match

Best Local Similarity 62.0%; Score 31.6; DB 2; Length 3901;

Best Local Similarity 89.5%; Pred. No. 0.98; 4; Indels 0; Gaps 0;

Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGATGAAGCTGAAGAGAGAGAGAGAGAGAGA 38

Db 3280 GAGGAGAGAGAGAGAGAGAGATGAGAGAGAGAGA 3317

RESULT 19

US-09-357-014-6

Sequence 6, Application US/09357014

Patent No. 6291645

GENERAL INFORMATION:

APPLICANT: Jaekyoon Shin, Insil Joungh, Ratna K. Vadlamudi

and Jack L. Strominger

TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES

AND USUS THEREFOR

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/357,014

FILING DATE: 19-Jul-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/574,959

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: DFN-008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 3901 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 439..3847
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match

Best Local Similarity 62.0%; Score 31.6; DB 3; Length 3901;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGATGAGCTGAAGAGAGAGAGAGAGAGAGAGAGA 38

DB 3280 GAGGAGAGAGAGAGAGAGAGAGATGAGAGAGAGAGA 3317

RESULT 20

US-09-620-312D-480
Sequence 480, Application US/09620312D
Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, X. Tom

APPLICANT: Liu, Chenghua

APPLICANT: Neundl, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Chen, Rui-hong

APPLICANT: Zhao, Qing A.

APPLICANT: Wehrman, Tom

APPLICANT: Xue, Aiding J.

APPLICANT: Yang, Yonghong

APPLICANT: Wang, Jian-Rui

APPLICANT: Zhou, Ping

APPLICANT: Ma, Yuning

APPLICANT: Wang, Dunrui

APPLICANT: Wang, Zhimei

APPLICANT: John Tillinghast

APPLICANT: Dimanac, Radoje T.

TITLE OF INVENTION: No. 6569662el Nucleic Acids and

FILE REFERENCE: 784C1P2B

CURRENT APPLICATION NUMBER: US/09/620,312D

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

NUMBER OF SEQ ID NOS: 1105

SOFTWARE: pt_fl_genes Version 1.0

SEQ ID NO 480

LENGTH: 4226

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(2982)

US-09-620-312D-480

Query Match

Best Local Similarity 62.0%; Score 31.6; DB 4; Length 4226;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGGATGAGCTGAAGAGAGAGAGAGAGAGAGAGA 38

DB 658 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA 695

RESULT 21

US-09-345-882-4
Sequence 4, Application US/09345882
Patent No. 6393173

GENERAL INFORMATION:

APPLICANT: Bougueleret, Lydie

TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)

FILE REFERENCE: GENSET-031A

CURRENT APPLICATION NUMBER: US/09/345,882

PRIOR FILING DATE: 1999-06-30

PRIOR APPLICATION NUMBER: US 60/091,315

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/111,909

NUMBER OF SEQ ID NOS: 140

SOFTWARE: Patent.pm

SEQ ID NO 4

LENGTH: 6002

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: allele

LOCATION: 1319

OTHER INFORMATION: 5-130-257 : polymorphic base A or G

FEATURE:

NAME/KEY: allele

LOCATION: 1338

OTHER INFORMATION: 5-130-276 : polymorphic base A or G

FEATURE:

NAME/KEY: allele

LOCATION: 1944

OTHER INFORMATION: 5-136-174 : polymorphic base C or T

FEATURE:

NAME/KEY: allele

LOCATION: 3329

OTHER INFORMATION: 5-143-84 : polymorphic base A or G

FEATURE:

NAME/KEY: allele

LOCATION: 4582

OTHER INFORMATION: 5-148-352 : polymorphic base G or T

FEATURE:

NAME/KEY: allele

LOCATION: 1107..1125

OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33

FEATURE:

NAME/KEY: allele

LOCATION: 1107..1125

OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54

FEATURE:

NAME/KEY: allele

LOCATION: 1315..1338

OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35

FEATURE:

NAME/KEY: allele

LOCATION: 1315..1338

OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56

FEATURE:

NAME/KEY: allele

LOCATION: 1921..1967

OTHER INFORMATION: polymorphic fragment 5-136-174 SEQ ID41

FEATURE:

NAME/KEY: allele

LOCATION: 1921..1967

OTHER INFORMATION: polymorphic fragment 5-136-174 SEQ ID62

FEATURE:

NAME/KEY: allele

```

1 LOCATION: 3306..3352
2 OTHER INFORMATION: polymorphic fragment 5-143-84 SEQ ID46
3 FEATURE:
4 NAME/KEY: allele
5 LOCATION: 3306..3352
6 OTHER INFORMATION: polymorphic fragment 5-143-84 SEQ ID67
7 FEATURE:
8 NAME/KEY: allele
9 LOCATION: 1296..1338
10 OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
11 FEATURE:
12 NAME/KEY: allele
13 LOCATION: 1296..1338
14 OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
15 FEATURE:
16 NAME/KEY: allele
17 LOCATION: 3323..3369
18 OTHER INFORMATION: polymorphic fragment 5-143-101 SEQ ID45
19 FEATURE:
20 NAME/KEY: allele
21 LOCATION: 3323..3369
22 OTHER INFORMATION: polymorphic fragment 5-143-101 SEQ ID66
23 FEATURE:
24 NAME/KEY: allele
25 LOCATION: 4559..4605
26 OTHER INFORMATION: polymorphic fragment 5-148-352 SEQ ID48
27 FEATURE:
28 NAME/KEY: allele
29 LOCATION: 4559..4605
30 OTHER INFORMATION: polymorphic fragment 5-148-352 SEQ ID69
31 FEATURE:
32 NAME/KEY: misc_feature
33 LOCATION: 442..444
34 OTHER INFORMATION: ATG
35 FEATURE:
36 NAME/KEY: misc_feature
37 LOCATION: 4378..4380
38 OTHER INFORMATION: stop : TGA
39 FEATURE:
40 NAME/KEY: polyA_signal
41 LOCATION: 4878..4883
42 OTHER INFORMATION: potential
43 FEATURE:
44 NAME/KEY: polyA_signal
45 LOCATION: 5116..5121
46 OTHER INFORMATION: potential
47 FEATURE:
48 NAME/KEY: polyA_signal
49 LOCATION: 5896..5901
50 OTHER INFORMATION: potential
51 FEATURE:
52 NAME/KEY: polyA_signal
53 LOCATION: 5981..5986
54 FEATURE:
55 NAME/KEY: misc_feature
56 LOCATION: 209..756
57 OTHER INFORMATION: homology with EST in ref emb1:W84531
58 FEATURE:
59 NAME/KEY: misc_feature
60 LOCATION: 391..815
61 OTHER INFORMATION: complement homology with EST in ref emb1:W37603
62 FEATURE:
63 NAME/KEY: misc_feature
64 LOCATION: 453..898
65 OTHER INFORMATION: complement homology with EST in ref emb1:H39516
66 FEATURE:
67 NAME/KEY: misc_feature
68 LOCATION: 818..1306
69 OTHER INFORMATION: complement homology with EST in ref emb1:W67770
70 FEATURE:
71 NAME/KEY: misc_feature
72 LOCATION: 844..1303
73 OTHER INFORMATION: complement homology with EST in ref emb1:AA2624227

```

```

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1351..1702
OTHER INFORMATION: complement homology with EST in ref embl:AA485189
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1866..2109
OTHER INFORMATION: homology with EST in ref embl:AA296993
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2181..2281
OTHER INFORMATION: homology with EST in ref embl:T61718
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2253..2482
OTHER INFORMATION: homology with EST in ref embl:AA082927
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2480..2842
OTHER INFORMATION: complement homology with EST in ref embl:H38607
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3334..3733
OTHER INFORMATION: homology with EST in ref embl:AA279595
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3631..3870
OTHER INFORMATION: complement homology with EST in ref embl:AA169631
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3883..4421
OTHER INFORMATION: homology with EST in ref embl:H08612
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4277..4796
OTHER INFORMATION: homology with EST in ref embl:AA399016
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4516..5016
OTHER INFORMATION: homology with EST in ref embl:AA479433
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5580..6002
OTHER INFORMATION: complement homology with EST in ref embl:AA167428
US-09-345-882-4

Query Match          62.0%  Score 31.6;  DB 4;  Length 6002;
Best Local Similarity 89.5%  Pred. No. 1;
Matches 34;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;

Cy      1  GAGCATGAAGCTGAAGAGAGAGAGAGAGAGAGA 38
      |||||
Db      2056 GATGAAGAAGCAGAAAGAGAGAGAGAGAGAGA 2053

RESULT 22
US-09-345-882-1
Sequence 1, Application US/09345882
Patent No. 6399373
GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
SEQ ID NO 1

```

```

1 LOCATION: 146328
2 OTHER INFORMATION: 5-143-84 : polymorphic base A or G
3 FEATURE:
4 NAME/KEY: allele
5 LOCATION: 146345
6 OTHER INFORMATION: 5-143-101 : polymorphic base A or C
7 FEATURE:
8 NAME/KEY: allele
9 LOCATION: 150329
10 OTHER INFORMATION: 5-145-24 : polymorphic base A or G
11 FEATURE:
12 NAME/KEY: allele
13 LOCATION: 160031
14 OTHER INFORMATION: 5-148-352 : polymorphic base G or T
15 FEATURE:
16 NAME/KEY: allele
17 LOCATION: 72771..72817
18 OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
19 FEATURE:
20 NAME/KEY: allele
21 LOCATION: 72771..72817
22 OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID31
23 FEATURE:
24 NAME/KEY: allele
25 LOCATION: 88050..88096
26 OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID51
27 FEATURE:
28 NAME/KEY: allele
29 LOCATION: 88050..88096
30 OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
31 FEATURE:
32 NAME/KEY: allele
33 LOCATION: 90819..90865
34 OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
35 FEATURE:
36 NAME/KEY: allele
37 LOCATION: 90819..90865
38 OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
39 FEATURE:
40 NAME/KEY: allele
41 LOCATION: 93690..93736
42 OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
43 FEATURE:
44 NAME/KEY: allele
45 LOCATION: 93690..93736
46 OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
47 FEATURE:
48 NAME/KEY: allele
49 LOCATION: 97099..97145
50 OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
51 FEATURE:
52 NAME/KEY: allele
53 LOCATION: 97099..97145
54 OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
55 FEATURE:
56 NAME/KEY: allele
57 LOCATION: 97130..97177
58 OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
59 FEATURE:
60 NAME/KEY: allele
61 LOCATION: 97130..97177
62 OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
63 FEATURE:
64 NAME/KEY: allele
65 LOCATION: 99075..99121
66 OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
67 FEATURE:
68 NAME/KEY: allele
69 LOCATION: 99075..99121
70 OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
71 NAME/KEY: allele
72 LOCATION: 99094..99140

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: OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
: FEATURE:
: NAME/KEY: allele
: LOCATION: 99094..99140
: OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
: FEATURE:
: NAME/KEY: allele
: LOCATION: 103783..103828
: OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
: FEATURE:
: NAME/KEY: allele
: LOCATION: 103783..103828
: OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
: FEATURE:
: NAME/KEY: allele
: LOCATION: 106918..106966
: OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
: FEATURE:
: NAME/KEY: allele
: LOCATION: 106918..106966
: OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108084..108130
: OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108084..108130
: OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108127..108177
: OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
: FEATURE:
: NAME/KEY: allele
: LOCATION: 108127..108177
: OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
:
Query Match 62.0% Score 31.6 DB 4 Length 162450;
Best Local Similarity 89.5% Pred. No. 1.4;
Matches 34; Conservative 0; Mismatches 4; Indels 0; Gaps 0
OY 1 GAGGTGAAGCTGAAGAGAGAGAGAGAGAGAGAGA 38
Db 114367 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGA 114404
:
RESULT 23
US-09-817-310-1
: Sequence 1, Application US/09817310
: Patent No. 653431
: GENERAL INFORMATION:
: APPLICANT: Stewart, Mary
: APPLICANT: Kozma, Sarah
: TITLE OF INVENTION: Drosophila Melanogaster P70 S6 Kinase
: FILE REFERENCE: 4-20971/A
: CURRENT APPLICATION NUMBER: US/09/817,310
: PRIOR APPLICATION NUMBER: 09/230,247
: PRIOR FILING DATE: 1999-04-16
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 2556
: TYPE: DNA
: ORGANISM: Drosophila melanogaster
US-09-817-310-1
Query Match 61.6% Score 31.4 DB 4 Length 2556;
Best Local Similarity 77.6% Pred. No. 1.1;
Matches 38; Conservative 0; Mismatches 11; Indels 0; Gaps 0

```

```

OY      2 AGGATGAAGCTGAAGAAGAGAGAGAGAGAAAGTGTGAACCCCA 50
        ||||| | | | | | | | | | | | | | | | | | | | | |
DB      2161 ACGAGTGTCGGAGAGAGAGAGAGAGAGAGAGAGAGCCTGTACACACA 2209

RESULT_24
US-09-702-705-309/c
; Sequence 309, Application US/09702705.
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478CI4
CURRENT APPLICATION NUMBER: US/09/702.705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 309
LENGTH: 129
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(129)
OTHER INFORMATION: n = A,T,C or G
US-09-702-705-309

Query Match          61.2%; Score 31.2; DB 4; Length 129;
Best Local Similarity 81.8%; Pred. No. 0.94;
Matches    36; Conservative   0; Mismatches     8; Indels       0; Gaps       0;

OY      1 GAGATGAAGCTGAAGAAGAGAGAGAGAGAGAAGTGTGA 44
        ||||| | | | | | | | | | | | | | | | | | |
DB      106 GAGGAGAAGGTGGGAGAGAGAGAGAGAGAGAGAAGACTGA 63

RESULT_25
US-09-736-457-309/c
; Sequence 309, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478CI5
CURRENT APPLICATION NUMBER: US/09/736.457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 309
LENGTH: 129
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
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DY 1 GAGCATTAACGTGAAGAGGAGGAGGAGGAGGAGACTGTCA 44
| | | | |
Db 206 GAGGAAGAAGTGGGAGGAAAGGAGGAGGAGAAAGCTCA 63

```

GENERAL INFORMATION:
PATENT NO. 6630574
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannich, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 309
LENGTH: 129
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(125)
OTHER INFORMATION: n = A,T,C or G
US-09-614-124B-309

```

Matches	36; Conservative	0; Mismatches	8; Indels	0; Gaps	0;
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Dy
1 GAGGATGAACCTGAAGAGGAGGAGGAGCGAAGCAAGTGTGA 44

Db
106 GAGGAAGAAGTGCCGGAGGAAGAGGACGAGGAAGAAGAGGTGA 63

Sequence 309, Application US/09671325
Patent No. 6667154
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Iodes, Michael A.
APPLICANT: Panger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825

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; ORGANISM: Homo sapien
;
; FEATURE:
;
; NAME/KEY: misc_feature
; LOCATION: (1) .. (129)
; OTHER INFORMATION: n = A,T,C or G
US-09-671-325-309

```

QY 1 GAGATGAAGCTGAAGCAGCAGCAGCAGCAGAAAGCTGTGA 44
 |||||
 Db 106 GAGGAGAAAGTGGGAGAGAAAGCAGCAGCAGAAAGAAAGCTGA 63
 |||||

RESULT 28
US-09-589-184-309/c
; Sequence 309, Application US/09589184
; Patent No. 6686447

```

1  APPLICANT:  Wang, Tongtong
2  APPLICANT:  Bangur, Chaitanya S.
3  APPLICANT:  Lodes, Michael A.
4  APPLICANT:  Fanger, Gary
5  APPLICANT:  Vedvik, Tom
6  APPLICANT:  Carter, Darick
7  APPLICANT:  Retter, Marc
8  APPLICANT:  Mannion, Uane
9  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THERAPY AND
10 TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
11 FILE REFERENCE:  210121.478C8
12 CURRENT APPLICATION NUMBER:  US/09/569,184
13 NUMBER OF FILING DATE:  2000-06-05
14 SOFTWARE:  FastSeq for Windows Version 3.0
15 SEQ ID NO 309
16 LENGTH:  129

```

```

; ORGANISM: Homo sapien
;
; FEATURE:
;
; NAME/KEY: misc_feature
; LOCATION: (1) .. (129)
; OTHER INFORMATION: n = A,T,C or G
US-09-589-184-309

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```
Query Match          61.2%; Score 31.2; DB 4; Length 129;
Best Local Similarity 81.8%; Pred. No. 0.94;
Matches 36; Conservative 0; Mismatches 8. Total 44
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OY 1 GAGCATGAACCTGAAAGAGAGAGAGAGAGAGAAGACTGTCA 4
 ||||| ||||| ||||| ||||| ||||| |||||
Dδ 106 GAGCAGAAGGTTGGGAGAGAAAGAGAGAGAGAGAAGAAGTGA 6

RESULT 29
US-09-621-976-18731
; Sequence 18731, Application US/09621976
; Patent No. 6639063

1 GENERAL INFORMATION:
2 APPLICANT: Dumas Milne Edwards, J.B.
3 APPLICANT: Jobert, S.
4 APPLICANT: Giordano, J.Y.
5 TITLE OF INVENTION: ESTs and Encoded Human Proteins
6 FILE REFERENCE: GENSET 054P2
7 CURRENT APPLICATION NUMBER: US/09/621,976
8 CURRENT FILING DATE: 2000-07-21
9 NUMBER OF SEQ ID NOS: 19335
10 SOFTWARE: Patent.pm


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; SEQ ID NO 18731
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-18731

```

Query Match	61.2%	Score 31.2	DB 4	length 403
Best Local Similarity	81.8%	Pred. No. 1		
Matches 36	Conservative 0	Mismatches 8	Indels 0	Gaps 0

OY 1 GAGCATGAAGCTGAAAGAGGAGCAGCAGGAGGAAGTGTGA 44
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 341 GAGGAAGAAGTTGGGAGGAGAGGAGGAGGAAGAAGAACGTGA 384

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RESULT 30
US-09-621-976-18711
; Sequence 18711, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: EST's and Encoded Human Proteins.
; FILE REFERENCE: GENSET. 054PR2
; CURRENT APPLICATION NUMBER: US/09/621, 976
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18711
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 72..215..229
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-18711

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Query Match	61.2%	Score 31.2;	DB 4;	Length 427;
Best Local Similarity	81.8%	Pred. No. 1;		
Matches 36;	Conservative	0;	Mismatches 8;	Indels 0;
				Gaps 0;

Oy 1 GAGGATGAAGCTGAAAGAGCGAGGAGGAGGAAGACTGTGA 44
| | | | |
Db 343 GAGGAAGAAGTGGCGAGGAAGAAGAGAGGAAGAAGAAGTGA 386

Search completed: February 29, 2004, 22:26:08
Job time : 65.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 20:09:29 ; Search time 197 Seconds
(without alignments)
933.913 Million cell updates/sec

Title: US-09-692-077D-2_COPY_880_930

Perfect score: 51

Sequence: 1 gagagtgagctgaagagga.....aggaagagtgtgaccaccag 51

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2353733 seqs, 180373377 residues

Total number of hits satisfying chosen parameters: 4707466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 150 summaries

Database : Published Applications NA.*

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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	51	100.0	1344 14	US-10-001-073-2 Sequence 2, Appl1
2	47.8	93.7	1344 14	US-09-825-923-1 Sequence 1, Appl1
3	47.8	93.7	1344 14	US-10-077-870-1 Sequence 1, Appl1
4	41.8	82.0	6804 14	US-10-311-455-47 Sequence 47, Appl1
5	41.6	81.6	1353 9	US-09-825-923-3 Sequence 3, Appl1
6	41.6	81.6	1353 14	US-10-077-870-3 Sequence 3, Appl1
7	41.6	81.6	1353 14	US-10-001-073-1 Sequence 1, Appl1
8	41.6	81.6	1353 14	US-10-305-720-1181 Sequence 1181, Ap
9	41.6	81.6	1353 14	US-10-225-567A-41 Sequence 41, Appl1
10	36	70.6	2367 14	US-10-128-714-6204 Sequence 6204, Ap
11	36	70.6	2367 14	US-10-128-714-7204 Sequence 7204, Ap
12	36	70.6	4338 14	US-10-128-714-204 Sequence 204, App
13	35.6	68.8	1012 12	US-10-128-714-5204 Sequence 5204, Ap
14	34.8	68.2	1554 12	US-10-424-599-139707 Sequence 139707, A
15	34.8	68.2	1554 12	US-10-424-599-94653 Sequence 94653, A

16	34.4	67.5	392 11	US-09-864-408A-1111 Sequence 1111, Ap
17	34.4	67.5	6628 15	US-10-191-803-61 Sequence 61, Appl1
18	33.8	66.3	182 9	US-09-844-864-12 Sequence 12, Appl1
19	33.8	66.3	1018 9	US-09-844-864-5 Sequence 5, Appl1
20	33.8	66.3	2526 12	US-10-424-599-108927 Sequence 108927, A
21	33.8	66.3	3401 15	US-10-369-493-27799 Sequence 27799, A
22	33.4	65.5	2981 14	US-10-205-194-145 Sequence 145, App
23	33.2	65.1	193 9	US-09-864-761-23094 Sequence 23094, A
24	33.2	65.1	477 10	US-09-918-995-27029 Sequence 27029, A
25	33.2	65.1	492 9	US-09-864-761-63788 Sequence 6378, Ap
26	33	64.7	390 15	US-10-242-555A-43536 Sequence 43536, A
27	33	64.7	650 9	US-09-879-536-333 Sequence 333, App
28	32.8	64.3	1634 12	US-10-424-599-60174 Sequence 60174, A
29	32.8	64.3	150 14	US-10-029-386-18468 Sequence 18468, A
30	32.8	64.3	223 9	US-09-728-444-146 Sequence 146, App
31	32.8	64.3	253 9	US-09-728-445-59 Sequence 59, Appl1
32	32.8	64.3	333 14	US-10-029-386-13715 Sequence 13715, A
33	32.8	64.3	336 15	US-10-085-117-303 Sequence 303, App
34	32.8	64.3	410 9	US-09-960-352-13656 Sequence 13656, A
35	32.8	64.3	525 14	US-10-029-386-4712 Sequence 4712, Ap
36	32.8	64.3	583 15	US-10-027-632-104255 Sequence 104255, A
37	32.8	64.3	583 15	US-10-027-632-325232 Sequence 325232, A
38	32.8	64.3	585 14	US-10-029-386-8 Sequence 8, Appl1
39	32.8	64.3	1191 15	US-10-085-117-302 Sequence 302, App
40	32.8	64.3	1760 12	US-10-221-625-169 Sequence 169, App
41	32.8	64.3	1845 14	US-10-029-386-24791 Sequence 24791, A
42	32.8	64.3	2336 15	US-10-320-797-2216 Sequence 2216, Ap
43	32.8	64.3	3346 15	US-10-320-797-1316 Sequence 1316, Ap
44	32.8	64.3	5346 15	US-10-320-797-1316 Sequence 316, App
45	32.8	64.3	5387 13	US-10-001-873-22 Sequence 22, Appl1
46	32.8	64.3	23861 15	US-10-085-117-301 Sequence 301, Appl1
47	32.8	64.3	6833 15	US-10-034-650-301 Sequence 31, Appl1
48	32.8	64.3	158405 14	US-10-175-522-86 Sequence 86, Appl1
49	32.8	64.3	3186778 15	US-10-027-632-174961 Sequence 174961, A
50	32.6	63.9	118 9	US-09-864-761-29612 Sequence 29612, A
51	32.6	63.9	330 9	US-09-728-444-124 Sequence 124, App
52	32.6	63.9	596 9	US-09-864-761-11050 Sequence 13050, A
53	32.6	63.9	661 9	US-09-894-998-34 Sequence 34, Appl1
54	32.6	63.9	661 14	US-10-121-998-34 Sequence 34, Appl1
55	32.6	63.9	661 14	US-10-200-562-34 Sequence 34, Appl1
56	32.6	63.9	661 14	US-10-237-551-34 Sequence 34, Appl1
57	32.6	63.9	755 12	US-10-424-559A-24281 Sequence 24281, A
58	32.6	63.9	1949 14	US-10-029-386-22897 Sequence 22897, A
59	32.6	63.9	2445 14	US-10-157-031-23 Sequence 23, Appl1
60	32.4	63.5	243 9	US-09-864-761-26712 Sequence 26712, A
61	32.4	63.5	253 12	US-10-424-559A-15464 Sequence 15464, A
62	32.4	63.5	362 9	US-09-864-761-10070 Sequence 10070, A
63	32.4	63.5	1570 9	US-09-801-574-50 Sequence 50, Appl1
64	32.4	63.5	1995 9	US-09-925-300-441 Sequence 441, Appl1
65	32.4	63.5	6483 9	US-09-880-107-3699 Sequence 3699, Ap
66	32.4	63.5	6483 15	US-10-435-636-24 Sequence 24, Appl1
67	32.2	63.1	231 15	US-10-242-555A-7014 Sequence 7014, Ap
68	32.2	63.1	280 15	US-10-242-555A-53932 Sequence 53932, A
69	32.2	63.1	336 15	US-10-242-555A-14445 Sequence 14445, A
70	32.2	63.1	340 15	US-10-242-555A-8756 Sequence 8756, Ap
71	32.2	63.1	384 14	US-10-029-386-22429 Sequence 22429, A
72	32.2	63.1	386 9	US-09-925-300-817 Sequence 817, App
73	32.2	63.1	388 15	US-10-242-555A-22486 Sequence 22486, A
74	32.2	63.1	393 10	US-09-803-719-2236 Sequence 2236, Ap
75	32.2	63.1	426 12	US-10-425-114-21268 Sequence 21268, A
76	32.2	63.1	427 9	US-09-815-343-1075 Sequence 1075, Ap
77	32.2	63.1	430 14	US-10-115-712-178 Sequence 178, App
78	32.2	63.1	473 15	US-10-242-555A-86235 Sequence 26335, A
79	32.2	63.1	477 9	US-09-864-761-286 Sequence 286, App
80	32.2	63.1	497 9	US-09-864-761-287 Sequence 287, App
81	32.2	63.1	497 9	US-09-796-692-9443 Sequence 9443, Ap
82	32.2	63.1	491 14	US-10-040-862-9443 Sequence 9443, Ap
83	32.2	63.1	491 15	US-10-057-455B-9443 Sequence 9443, Ap
84	32.2	63.1	491 15	US-10-154-864B-9443 Sequence 9443, Ap
85	32.2	63.1	562 14	US-10-029-386-8701 Sequence 8701, Appl1
86	32.2	63.1	648 14	US-10-300-072-32 Sequence 32, Appl1
87	32.2	63.1	752 14	US-10-029-386-20898 Sequence 20898, A
88	32.2	63.1	1173 15	US-10-161-927-81 Sequence 81, Appl1


```

RESULT 12
US-10-128-714-204
; Sequence 204, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE OF INVENTION: Methode of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
; LENGTH: 4238
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-204
Query Match 70.6%, Score 36, DB 14, Length 4238,

```

```

RESULT 14
US-10-424-599-139707
; Sequence 139707, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 139707
; LENGTH: 1012
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97163C.1
US-10-424-599-139707

```


RESULT 19
 US-09-844-864-5
 : Sequence 5, Application US/03944864
 : Patent No. US20020042926A1
 : GENERAL INFORMATION:
 : APPLICANT: Matzuk, Martin
 : APPLICANT: Ren, Yongsheng
 : APPLICANT: Mu, Xuemei
 : TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
 : FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
 : CURRENT APPLICATION NUMBER: 2001-04-27
 : PRIOR FILING DATE: 1998-10-28
 : PRIOR APPLICATION NUMBER: PCT/US99/25209
 : PRIOR FILING DATE: 1999-10-28
 : NUMBER OF SEQ ID NOS: 25
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 5
 : LENGTH: 1018
 : TYPE: DNA
 : ORGANISM: Mus musculus
 : US-09-844-864-5
 :
 Query Match 66.3%, Score 33.8; DB 9; Length 1018;
 Best Local Similarity 84.4%; Pred. No. 0.18;
 Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGTGTGAA 45
 |||||||
 Db 528 GAAAGATGACGAGGAAGAGGAGGAGGAGGAGGAGGATGAA 572
 |||||||

RESULT 20
 US-10-424-599-108927
 : Sequence 108927, Application US/10424599
 : Publication No. US20040031072A1
 : GENERAL INFORMATION:
 : APPLICANT: La Rosa Thomas J
 : APPLICANT: Kovalic David K
 : APPLICANT: Zhou Yihua
 : APPLICANT: Cao Yongwei
 : TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 : TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 : FILE REFERENCE: 38-21(53223)B
 : CURRENT APPLICATION NUMBER: US/10/424,599
 : CURRENT FILING DATE: 2003-04-28
 : NUMBER OF SEQ ID NOS: 285684
 : SEQ ID NO 108927
 : LENGTH: 2526
 : TYPE: DNA
 : ORGANISM: Glycine max
 : FEATURE:
 : OTHER INFORMATION: Clone ID: PAT_MRT3847_69375C.1
 : US-10-424-599-108927
 :
 Query Match 66.3%, Score 33.8; DB 12; Length 2526;
 Best Local Similarity 84.4%; Pred. No. 0.18;
 Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGTGTGAA 45
 |||||||
 Db 1420 GAAAGAGGAAGAGGAAGAGGAGGAGGAGGAGGAGGAGTGA 1464
 |||||||

RESULT 21
 US-10-369-493-27799
 : Sequence 27799, Application US/10369493
 : Publication No. US20030233675A1
 : GENERAL INFORMATION:
 : APPLICANT: Cao, Yongwei
 : APPLICANT: Hinkle, Gregory J.
 :

```

; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIORITY FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 27799
LENGTH: 3401
TYPE: DNA
ORGANISM: Neurospora crassa
US-10-369-493-27799

Query Match      66.3%; Score 33.8; DB 15; Length 3401;
Best Local Similarity 84.4%; Pred. No. 0.18;
Matches 38; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY      1 GAGATGAAGCTGAAAGAGAGAGAGAGAGAGAGTGTGAA 45
Db      3129 GAGATGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGTAGCGA 3173
|||||
|||||

RESULT 22
US-10-205-194-145
; Sequence 145, Application US/10205194
; Publication No. US20030134301A1
GENERAL INFORMATION:
APPLICANT: Warner-Lambert Company
APPLICANT: Lee, Kevin
APPLICANT: Dixon, Alistair
APPLICANT: Brooksbank, Robert
APPLICANT: Pincock, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
FILE REFERENCE: WL-A-018201
CURRENT APPLICATION NUMBER: US/10/205,194
CURRENT FILING DATE: 5200-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 177
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 145
LENGTH: 2981
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: RNAI homolog
US-10-205-194-145

Query Match      65.5%; Score 33.4; DB 14; Length 2981;
Best Local Similarity 78.4%; Pred. No. 0.24;
Matches 40; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY      1 GAGATGAAGCTGAAAGAGAGAGAGAGAGAGAGTGTGACCCG 51
Db      1427 GAAGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCCTCG 1477
|||||
|||||

RESULT 23
US-09-864-761-23094
; Sequence 23094, Application US/09864761
; Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Neomica-X-1

```

us-09-692-077d-2-copy-880-930.rnpb

```

CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00674
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1
SEQ ID NO 23094
LENGTH: 193

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```

US-09-864-761-22094      Other
US-09-864-761-22094      US-09-864-761-22094
Query Match                65.1% ; Score 33.2; DB 9; Length 193;
Similarity                 92.1%; Pred. No. 0.28; 3; Indels 0; Gaps 0
Best Local                  0; Mismatches 39
Matches                     35; Conservative
2 AGATGAAGCTCGAAGAGGAGGAGGAGGAGGAGGAGGAG 120
| | | | | | | | | | | | | | | | | | | | |
83 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
Db
RESULT 24
US-09-918-995-27029
; Sequence 27029, Application US/09918995
; Publication No. US20030073623M1
; GENERAL INFORMATION

```

[illegible]

RESULT 25
US-09-864-761-6378, Application US/09864761
Sequence 6378, Application US/09864763A1
Patent No. US2002048763A1
GENERAL INFORMATION
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenhang
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
SITE REFERENCE: Aecmla-x-1
CURRENT FILING DATE: 2001-05-23
CURRENT FILING DATE: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/02-04
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30

```

1  PRIOR APPLICATION NUMBER: US 09/774,203
2  PRIOR FILING DATE: 2001-01-29
3  NUMBER OF SEQ ID NOS: 49117
4  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
5  SEQ ID NO 6378
6  LENGTH: 492
7  TYPE: DNA
8  ORGANISM: Homo sapiens
9  FEATURE:
10 OTHER INFORMATION: MAP TO AC004687.1
11 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
12 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3
13 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
14 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3
15 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
16 OTHER INFORMATION: EXPRESSED IN HEEL, SIGNAL = 2.8
17 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
18 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.6
19 US-09-864-761-6378

```

Query Match	65.1%	Score 33.2;	DB 9;	Length 492;
Best Local Similarity	92.1%;	Pred. No. 0.28;		
Matches 35;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;

OY 2 AGCATGAGCTGAAGAGGAGGAGGACGAGCAAGCAG 39
| | | | | | | | | | | | | | | | | | | | |
Db 367 AGAGGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAG 404

RESULT 26
US-10-242-535A-43536/c
; Sequence 43536, Application US/10242535A
; Publication No. US20040013663A1

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

```
1 FILE REFERENCE: 4231/2005
2 CURRENT APPLICATION NUMBER: US/10/242,535A
3 CURRENT FILING DATE: 2002-09-12
4
5 PRIOR APPLICATION NUMBER: US 10/085,763
6
7 PRIOR FILING DATE: 2002-02-28
8
9 PRIOR APPLICATION NUMBER: US 60/305,340
10
11 PRIOR FILING DATE: 2001-07-13
12
13 PRIOR APPLICATION NUMBER: US 60/275,017
14
15 PRIOR FILING DATE: 2001-03-12
16
17 PRIOR APPLICATION NUMBER: US 60/271,955
18
19 PRIOR FILING DATE: 2001-02-28
20
21 NUMBER OF SEQ ID NOS: 58994
22
23 SOFTWARE: PatentIn version 3.2
```

```

; SEQ ID NO 43536
;
; LENGTH: 390
;
; TYPE: DNA
;
; ORGANISM: Human
;
US-10-242-535A-43536

```

Query Match	64.7%	Score 33;	DB 15;	Length 390;
Best Local Similarity	79.6%	Pred. No. 0.32;		
Matches 39;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0

Oy 1 GAGGATGAACCTGAAGAGGAGGAGGAGAAGGTGTGAACCCC 49
 |||||
Db 185 GAGGAGGAAGAGGAGGAAGAGGAGGAGGAGCAGAAGAAACAC 137

RESULT 27
US-09-879-536-333

; GENERAL INFORMATION:
 ; APPLICANT: Endege, Wilson O.
 ; APPLICANT: Steinmann, Kathleen E.
 ; APPLICANT: Astle, Jon H.

```

APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/879,536
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/088, 801
PRIOR FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 333
LENGTH: 650
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc:feature
LOCATION: (1)..(650)
OTHER INFORMATION: n = A,T,C or G
US-09-879-536-333

```

Query Match	64.7%	Score 33;	DB 9;	Length 650;
Best Local Similarity	79.6%	Pred. No. 0.32;		
Matches 39;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;

OY 1 GAGGATGAACCTGAAGAAGAGGAGGAGGAGGAAAGTGTGAACCCC 49
 ||||| ||||| ||||| ||||| |||||
Db 245 GAGGAGCAAGAGGAAGAAGAGGAGGAGGAGGAGGAGGAAGAAAAC 293
 ||||| ||||| ||||| ||||| |||||

RESULT 28
US-10-424

```

1 sequence 60174, application US/10042553
2 Publication No. US20040031072A1
3 GENERAL INFORMATION:
4 APPLICANT: La Rosa Thomas J
5 APPLICANT: Kovalic David K
6 APPLICANT: Zhou Yihua
7 APPLICANT: Cao Yongwei
8 TITLE OF INVENTION: Soy Nucleic Acid N
9 TITLE OF INVENTION: Plants and Uses T
10 FILE REFERENCE: 38-21(51223) B
11 CURRENT APPLICATION NUMBER: US/10/424
12 CURRENT FILING DATE: 2003-04-28
13 NUMBER OF SEQ ID NOS: 285684
14 SEQ ID NO 60174

```

```

? LENGTH: 1634
?
? TYPE: DNA
?
? ORGANISM: Glycine max
?
? FEATURE:
?
? OTHER INFORMATION: clone ID: PAT_MRT3847_25349C.1
US-10-424-599-60174

```

Query Match	64.7%	Score 33	DB 12	Length 1634
Best Local Similarity	79.6%	Pred. No. 0.32		
Matches 39, Conservative	0	Mismatches 10	Indels 0	Gaps 0

OY

1 GAGGATGAAGCTGAAGAAGAGGAAGAAAGTGTGAACCC 49
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
D8 486 GAGGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAACCCC 53

RESULT 29
US-10-029-386-18468
; Sequence 18468, Application US/10029386
; Publication No. US20030194704A1

GENERAL INFORMATION:
 APPLICANT: Penn. Sharon G.
 David R. y
 SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

```

TYPE : DNA
ORGANISM : Homo sapiens
FEATURE : MAP TO AC011400.4 SIGNAL = 8.9
OTHER INFORMATION : EXPRESSED IN BONE MARROW, SIGNAL = 7.7
OTHER INFORMATION : EXPRESSED IN PLACENTA, SIGNAL = 8.4
OTHER INFORMATION : EXPRESSED IN ADULT LIVER, SIGNAL = 8.8
OTHER INFORMATION : EXPRESSED IN HEART, SIGNAL = 8.6
OTHER INFORMATION : EXPRESSED IN SKIN, SIGNAL = 8.3
OTHER INFORMATION : EXPRESSED IN TESTIS, SIGNAL = 8.1
US-10-029-386-14468    64 %   Score 32.8; DB 14; Length 150; Caps 0;
                        Pred. No. 0.38; ?; Indels      ;

```

Query Match	Similarity	84.1%	0;	Mismatch	45
Best Local	Conservative				
Matches	37;				72

[illegible]

RESULT 30
08-728-444-146
Application US/09728444

```

1  Patent No. US2007012071A1
2  General Information:
3  Applicant: Zambrotz, Brian
4  Applicant: Zambrotz, Arthur I
5  Applicant: Sande, No. US20020161207A1
6  Applicant: Sande, and Mutant Cells and Mutant Animals Defined Thereby
7  Title Of Invention:
8  Title Of Invention: LEX -0100-US# 09/728,444
9  File Reference:
10 File Reference: LEX -0100-US# 09/728,444
11 Current Filing Date: 2000-US 60/168,360
12 Current Application Number: 2000-US 60/168,360
13 Prior Filing Date: 1999-12-01
14 Prior Application Number: 1999-12-01
15 Number Of SEQ. ID NOS: 1206
16 Software: FASCSO for Windows Version 4.0
17 SEQ. ID NO 146
18 Length: 223

```

```

1 TYPE: DNA
2 ORGANISM: Mus musculus
3 FEATURE:
4 NAME/KEY: misc feature
5 LOCATION: (1)..(223)
6 OTHER INFORMATION: n = A,T,C or G
7
8 US-09-728-444-146
9
10 64.3% Score 32.8; DB 9; Length 223;
11 84.1% Pred. No 0.37; 7; Indels 0; Gaps 0
12 matches

```

Query Match	Similarity	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
Best Local	Similarity	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
Conservative	Similarity	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
Matches	Similarity	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99

[illegible]

Search completed: F
Top time 208 secs